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Effective filing tale	.6 pugen Ltd.	Search time 52 Seconds (without alignments) 48.902 Million pell upgates/sec				s: 1586107			of the result being printed, score distribution.  Description  Aab48919 Generic S Aab48919 SH2 domai Aab48925 SH2 domai Aab48926 SH2 domai Aab48938 SH2 domai Aab48937 SH2 domai
▼ Tue Jul 20 16:13:37 2004 □	GenCore version 5.1 Copyright (c) 1993 - 2004 Com	OM protein - protein search, using sw model Run on: July 20, 2004, 15:26:43 ; Search (with	Title: US-09-998-350-1 Perfect score: 45 seguence: 1 XLYENVGMY 9	Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5	hed: 1586107 segs, 282547505	Total number of hits satisfying chosen parameters Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Port-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Database : A_Geneseq_29Jan04:*  1. geneseq_29Jan04:*  2. geneseqp1980s:*  3. geneseqp2000s:*  4. geneseqp2001s:*  5. geneseqp2001s:*  6. geneseqp2003as:*  7. geneseqp2003as:*  8. geneseqp2003bs:*	Pred. No. is the number of results predicted score greater than or equal to the score of tand is derived by analysis of the total score of the coult score of the could be score

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to phosphotyrosine (pTyr)-containing regions of target proteins. The cyclic peptides are of one of the following formulae: Xaal-Leu2-Tyr3-Glu4-Assa-Val6-Gly7-Met8-Tyr9-NH where: Xaal is gamma-carboxy-Leu2-Tyr3-Kaad Assn5-Val6-Gly7-Met8-Car minoadipic acid (Aad, referred to as Adi in the specification); and Xaa3 is either Aad or Glu. Optionally, there is a conservative or neutral amino acid substitution at either to both of Leu2 and Gly7, and coptionally one or more of Tyr3, Glu4, Val6, Met8 and Tyr9 is modified.

The peptides are cyclised via a bridging moiety of the formula C(O)-CH2-Z CH2(O)NH2, where Z is sulphur, sulphoxide, oxygen or methylene, which links the nitrogen atom of the N terminus to the nitrogen atom of the N terminus to the nitrogen atom of the Araget protein is Grb2 (growth of Leuca receptor-bound protein 2). On binding Grb2, the peptides have a turn conformation. The peptides, and compositions comprising the peptides, are useful for inhibiting the binding of the SH2 domain to a target protein. They are particularly useful for preventing cancer, especially breast cancer. The present sequence is a generic representation of a cyclic peptide of the invention
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Inote = "The nitrogen atoms of the N-terminus and the C-terminal amide are joined via a bridging moiety, thereby cyclising the peptide"
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iive 0; Mismatches 0;
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The invention relates to redox-stable, non-phosphorylated cyclic peptides which bind to Src homology 2 (SH2) domains, preventing them from binding to phosphotyrosine (PTYP)-containing regions of target proteins. The cyclic peptides are of one of the following formulae: Xaal-Leu2-Tyr3-Glu4-Capalic peptides are of one of the following formulae: Xaal-Leu2-Tyr3-Glu4-Capalic peptides are of one of the following formulae: Xaal-Leu2-Tyr3-Glu4-Capalic peptides are of one of the following formulae: Xaal-Leu2-Tyr3-Glu4-Capalic acid (Aad, referred to as Adi in the specification); and Xaa2 is either Aad or Glu. Optionally, there is a conservative or neutral continuation at either or both of Leu2 and Gly7, and Xaa3 is coptionally one or more of Tyr3, Glu4, Val6, Met8 and Tyr9 is modified. The peptides are cyclised via bridging moiety of the formula C(0)-CH2-CC The peptides are cyclised via bridging moiety of the formula C(0)-CH2-CC CH2-CH(0)NE7, where Z is sulphur, sulphoxide oxygen or metrylene, which links the nitrogen atom of the N terminus to the nitrogen atom of the C-terminal amide. The peptides are characterised by an in vivo IC-50 of less than 4.0 micromolar when the target protein is GFD2 (growth C factor receptor-bound protein 2). On binding Grb2, the peptides have a curroconformation. They are particularly useful for preventing cancer, c especially breast cancer. The present sequence represents a cyclic especially breast cancer. The present sequence represents a cyclic especial content on the content of the invention.
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The invention relates to redox-stable, non-phosphorylated cyclic peptides which bind to Src homology 2 (SH2) domains, preventing them from binding to phosphotyroaline (pyry)-containing regions of target proteins. The cyclic peptides are of one of the following formulae: Xaal-leu2-Tyr3-Glu4-Cyclic peptides are of one of the following formulae: Xaal-leu2-Tyr3-Glu4-Cyclic peptides are of one of the following formulae: Xaal-leu2-Tyr3-Glu4-Cyclic peptides are of one of the following formulae: Xaal-leu2-Tyr3-Glu4-Cyclic Tyr9-NH where: Xaal is gamma-carboxy-lequtamic acid (Gla), Xaa2 is 2-caminoadipte and or Glu-Optionally, there is a conservative or neutral continually one or more of Tyr3, Glu4, Va16, Met8 and Tyr9 is modified. The peptides are cyclised via a bridging moiety of the formula C(O)-CH2-CHC(O)NH2, where Z is sulphux, sulphoxide, oxygan or methylene, which links the nitrogen atom of the N terminus to the nitrogen atom of the C-terminal amide. The peptides are characterised by an in vivo IC-50 of less than 4.0 micromolar when the target protein is GPD2 (growth C factor receptor-bound protein 2). On binding GPD2, the peptides have a turn conformation. The peptides, are useful for inhibiting the binding of the SH2 domain to a target protein. They are particularly useful for preventing cancer. Sepecially breast cancer. The present sequence represents a linear cycle precursor of a peptide of the invention
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Redox-stable, non-phosphorylated cyclic peptide inhibitors of the Src homology 2 domain binding to target protein, useful for preventing cancer, especially breast cancer.
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                                                                                                                                        Example 1; Page 13; 26pp; English
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Treatment or prophylaxis of a subject having a disorder characterized by

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                                                                                The invention relates to treatment or prophylaxis (M1) of a subject having a disorder characterised by abnormal interaction of Grb7 (Growth factor receptor-bound protein 7 and a Grb7 ligand, comprising administering to a subject in need of the treatment, a non-phosphorylated peptide comprising a sequence (S1, Tyr-Ala-Asn, Tyr-Glu-Asn and Tyr-Asp-Asn) or its functional equivalent, in an amount effective to inhibit the disorder. Also included are peptide antagonists/inhibitors of Grb7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1..10 /note= "The nitrogen atoms of the N-terminus and the C-terminal amide are joined via a bridging moiety, thereby cyclising the peptide"
                                                                                                                                                                                                      nucleic acids encoding the antagonists, an expression vector comprising the nucleic acid, a host cell transformed or transfected with the vector, screening (M2) a molecular library to identify a compound that inhibits interaction between Grb7 and a peptide antagonist and a phage display library comprising Grb7 antagonists. M1 is useful for prophylaxis or treatment of a subject having a disorder characterised by abnormal interaction of Grb7 and a Grb7 ligand, including breast or oesophageal
abnormal interaction of Grb7 and a Grb7 ligand, involves administering a non-phosphorylated peptide to a subject in need of the treatment.
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                                                                                                                                                                                                                                                                                                                           cancer, primary tumour or metastasis, or disorders in kidney, liver, gonads, breast, oesophagus, pancreas prostate, small intestine, placenta, colon, ovary, testes and lung. The present sequence is a G1 peptide (not defined) or derivative which is used to illustrate the possible structures of cyclic Grb7 antagonists
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SH2 domain binding inhibitor; non-phosphorylated; redox stable; cytostatic; tumour; breast cancer; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97.8%; Score 44; DB 5; Le
100.0%; Pred. No. 1.4e+06;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SH2 domain cyclic peptide inhibitor, SEQ ID NO:8.
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                                                     Disclosure; Fig 9B; 186pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9 AA;
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Best Local
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AAB48923
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The invention relates to redox-stable, non-phosphorylated cyclic peptides which bind to Src homology 2 (SH2) domains, preventing them from binding to posphotyrosine (Pyry)-containing regions of target proteins. The cyclic peptides are of one of the following formulae: Xaal-Leu2-Tyr3-Glu4-San5-Val6-Gly7-Met8-Tyr9-NH or Xaa2-Leu2-Tyr3-Xaa3-Asn5-Val6-Gly7-Met8-Tyr9-NH or Xaa2-Leu2-Tyr3-Xaa3-Asn5-Val6-Gly7-Met8-Tyr9-NH or Xaa2-Leu2-Tyr3-Xaa3-Asn5-Val6-Gly7-Met8-Tyr9-NH where: Xaal is gamma-carboxy-L-glutamic acid (Gla), Xaa2 is 2-minoadipic acid (Aad, referred to as Adi in the specification), and Xaa3 is either Aad or Glu. Optionally, there is a conservative or neutral amino acid substitution at either or both of Leu2 and Gly7, and optionally one or more of Tyr3, Glu4, Val6, Met8 and Tyr9 is modified. The peptides are cyclised via a bridging moiety of the formula C(O-CH2-CHC(O)MH2, where Z is sulphur, sulphoxide, oxygen or methylene, which links the nitrogen atom of the N terminus to the nitrogen atom of the C-cerminal anide. The peptides are characterised by an in vivo IC-So of less than 4.0 micromolar when the target protein is Grb2 (growth cator receptor-bound protein 2). On binding Gfb2, the peptides have a turn conformation. The peptides, and compositions comprising the peptides, are useful for inhibiting the binding of the SH2 domain to a carget protein. They are particularly useful for preventing cancer, especially breast cancer. The present sequence represents a cyclic peptide of the invention
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/note= "The nitrogen atoms of the N-terminus and the C-terminal amide are joined via a bridging moiety C(0)-CH2-S-CH2-CHC(0)NH2, thereby cyclising the peptide"
                                      Redox-stable, non-phosphorylated cyclic peptide inhibitors of the Src homology 2 domain binding to target protein, useful for preventing cancer, especially breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SH2 domain binding inhibitor, non-phosphorylated; redox stable, cytostatic; tumour; breast cancer; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97.8%; Score 44; DB 4; Length 10; 100.0%; Pred. No. 0.014; 0; Indels ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SH2 domain cyclic peptide inhibitor, SEQ ID NO:4.
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                                                                                                                     Example 2; Page 13; 26pp; English.
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  WPI; 2001-137633/14
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The invention relates to redox-stable, non-phosphorylated cyclic peptides which bind to Src homology 2 (SH2) domains, preventing them from binding to proper proteins of target proteins. The composition of the following formulae: Xaal-Leu2-Tyr3-Glu4-Asn5-Val6-Gly7-Met8-Tyr9-NH where: Xaal is gamma-carboxy-Leu2-Tyr3-Xaa3-Asn5-Val6-Gly7-Met8-Tyr9-NH where: Xaal is gamma-carboxy-Legituranic acid (Gla), Xaa2 is 2-aminoadipic acid (Aad, referred to as Adi in the specification); and Xaa3 is either Aad or Glu. Optionally, there is a conservative or neutral aminoadipic acid (Aad, referred to as Adi in the specification); and Xaa3 is either Aad or Glu. Optionally, there is a conservative or neutral continuation acid substitution at either or both of Leu2 and Gly7, and optionally one or more of Tyr3, Glu4, Val6, Met8 and Tyr9 is modified. The peptides are cyclised via a bridging moiety of the formula C(O)-CH2-C-CH2(O)MH2, where Z is sulphur, sulphoxide, oxygen or methylene, che C-terminal amide. The peptides are characterised by an in vivo IC-So factor receptor-bound protein 2). On binding Grb2, the peptides have a curn conformation. The peptides, and compositions comparising the peptides, are useful for inhibiting the binding of the SH2 domain to a carpet protein. They are particularly useful for preventing cancer, especially breast cancer. The present sequence represents a cyclic peptide of the invention
                                                                                                                            Redox-stable, non-phosphorylated cyclic peptide inhibitors of the Src homology 2 domain binding to target protein, useful for preventing cancer, especially breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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/note= "C-terminal amide, joined to a solid matrix"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SH2 domain binding inhibitor; non-phosphorylated; redox stable; cytostatic; tumour; breast cancer; linear precursor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97.8%; Score 44; DB 4; Length 10;
100.0%; Pred. No. 0.014;
ive 0; Mismatches 0; Indels
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                  (USSH ) US DEPT HEALTH & HUMAN SERVICES
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                                                        Lung FT,
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Best Local Similarity 100...
Best Local 8; Conservative
                                                      Long Y,
                                                                                            WPI; 2001-137633/14
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The invention relates to redox-stable, non-phosphorylated cyclic peptides which bind to Src homology 2 (SH2) domains, preventing them from binding to phosphotyroalne (PTyT)-containing regions of target proteins. The cyclic peptides are of one of the following formulae: Xaal-Leu2-Tyt3-Glu4 Cyclic peptides are of one of the following formulae: Xaal-Leu2-Tyt3-Glu4 CTyt9-NH where: Xaal is gamma-carboxy-Leu2-Tyt3-Xaa3-Asn5-Val6-Gly7-Wet8-CT Tyt9-NH where: Saal Leu2-Tyt3-Glu4 (Gla), Xaa2 is 2-amino-adipic acid (Aad, referred to as Adi in the specification); and Xaa3 is either Aad or Glu. Optionally, there is a conservative or neutral constitution at either or both of Leu2 and Gly7, and CCC The peptides are cyclised via a bridging moiety of the formula C(O)-CH2-Z (Ty2-CHC)(O)NH2, where Z is sulphoxide, wayge or methylene, which links the nitrogen atom of the N terminus to the nitrogen atom of the C-terminal amide. The peptides are characterised by an in vivo IC-50 of less than 4.0 micromolar when the target protein in vivo micromation. The peptides, and compositions comprising the currence for inhibiting the binding of the SH2 domain to a currence by a periode and compositions comprising the carget protein. They are particularly useful for preventing cancer. The presents a linear ceptersor of a peptide of the invention
                                                                                                            Redox-stable, non-phosphorylated cyclic peptide inhibitors of the Src homology 2 domain binding to target protein, useful for preventing cancer, especially breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SH2 domain binding inhibitor; non-phosphorylated; redox stable; cytostatic; tumour; breast cancer; linear precursor.
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100.0%; Pred. No. 0.014;
cive 0; Mismatches 0; Indels
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                                               Yang
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              (USSH ) US DEPT HEALTH & HUMAN SERVICES
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                                             Lung FT,
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                                                 Roller PP,
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The invention relates to redox-stable, non-phosphorylated cyclic peptides which bind to Src homology 2 (SH2) domains, preventing them from binding to phosphotyrosine (PTYP)-containing regions of target proteins. The cyclic peptides are of one of the following formulae: Xaal-Leuz-Tyr3-Glu4-Aan5-Val6-GlY7-Met8-Tyr9-NH or Xaa2-Leuz-Tyr3-Aan3-Aan5-Val6-GlY7-Met8-Tyr9-NH or Xaa2-Leuz-Tyr3-Aan3-Aan5-Val6-GlY7-Met8-Tyr9-NH or Xaa2-Leuz-Tyr3-Aan3-Aan5-Val6-GlY7-Met8-Tyr9-NH hare is a conservative or neutral aminoadipic acid (Au. Optionally, there is a conservative or neutral conservative or neutral amino acid substitution at either or both of Leuz and Aly7, and Xaa3 (The peptides are cyclised via a bridging moiety of the formula C(O)-CH2-C (The peptides are cyclised via a bridging moiety of the formula C(O)-CH2-C (The peptides are cyclised via a bridging moiety of the formula C(O)-CH2-C (The CHCO)NIX, where Z is sulphur, sulphoxide cycle or metrylene, which links the nitrogen atom of the N terminus to the nitrogen atom of the C-terminal amide. The peptides are characterised by an in vivo IC-50 of less than 4.0 micromolar when the target brotein is GFD2 (Growth C factor receptor-bound protein 2). On binding GFD2, the peptides have a currence of a peptides, are useful for inhibiting the binding of the SH2 domain to a target protein. They are particularly useful for preventing cancer, c especially breast cancer. The presents a linear ceptors of a peptide of the invention
                                                                                            Redox-stable, non-phosphorylated cyclic peptide inhibitors of the Src homology 2 domain binding to target protein, useful for preventing cancer, especially breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= Aad
/note= "C-terminal amide, joined to a solid matrix"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SH2 domain binding inhibitor; non-phosphorylated; redox stable; cytostatic; tumour; breast cancer; linear precursor.
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Pred. No. 0.014;
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                              King CR,
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                                                                                                                                                                            Example 1; Page 12; 26pp; English
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                             ĔΤ,
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                                Lung
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                              Roller PP, Long Y,
                                                                 4PI; 2001-137633/14
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nes 8; Conserv
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Modified-site
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Matches
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Gaps

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97WO-US012501
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                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 8; Conservative
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              WPI; 1998-110340/10.
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                                                                                                                                                                                                                                                                                                                                                         Sequence 11 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
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                                                                                                                                                                     The invention relates to redox-stable, non-phosphorylated cyclic peptides which bind to Src homology 2 (8H2) domains, preventing them from binding to properly of target proteins. The cyclic peptides are of one of the following formulae: Kaal-Leu2-Tyr3-Glu4-Asn5-Val6-Gly7-Met8-Tyr9-NH or Xaa2-Leu2-Tyr3-Xaa3-Asn5-Val6-Gly7-Met8-Tyr9-NH where: Xaal is gamma-carboxy-Lejutamic acid (Gla), Xaa2 is 2-aminoadipic acid (Aad, referred to as Adi in the specification); and Xaa3 aminoadipic acid (Aad, referred to as Adi in the specification); and Xaa3 aminoadipic acid (Aad, substitution at either or both of Leu2 and Gly7, and optionally one or more of Tyr3, Glu4, Val6, Met8 and Tyr9 is modified. The peptides are cyclised via a bridging moiety of the formula C(0)-CH2-Z CHC(0)MH2, where I is sulpiur, sulphoxide, oxygen or methylene, which links the nitrogen atom of the N terminus to the nitrogen atom of the C-terminal amide. The peptides are characterised by an in vivo IC-SO of less than 4.0 micromolar when the target protein is Grb2 (growth factor receptor-bound protein 2). On binding Gb2, the peptides have a turn conformation. The peptides, and compositions comprising the peptides, are useful for inhibiting the binding of the SH2 domain to a turn conformation. The preptides, and compositions comprising the peptides, are useful for inhibiting the binding of the SH2 domain to a target protein. They are particularly useful for preventing cancer, especially breast cancer. The present sequence represents a linear procured the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                src homology 2 domain; SH2 domain; Grb2;
non-phosphorylated; inhibition; treatment;
human cancer.
                                                                                 Redox-stable, non-phosphorylated cyclic peptide inhibitors of the Src homology 2 domain binding to target protein, useful for preventing cancer, especially breast cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 44; DB 4;
Pred. No. 0.014;
0; Mismatches
                             Yang
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(UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.
                            King CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oligino L;
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                               Example 5; Page 15; 26pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW46897 standard; peptide; 11 AÅ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97.8%; Scor
100.0%; Pro
                            FT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SHC phosphopeptide; binding; signal transduction protein; hyper-proliferative disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Krag D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97WO-US012501
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                            Lung
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LYENVGMY 9
                                                        WPI; 2001-137633/14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 LYENVGMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10 AA;
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The present sequence represents a peptide designated GIC-S. This peptide is essentially the same as a non-phosphorylated peptide, GI, that is capable of binding to the src homology 2 (SH2) domain of Grb2, except that the terminal Cys residues of GI are replaced with Ser residues. Grb2 peptide with Grb2 was tested, and it was demonstrated that the disulphide bond of GI may be important. The binding affinity of the present peptide with Grb2 was tested, and it was demonstrated that the disulphide bond of GI may be important. The GI peptide binds to the SH2 domain of phosphopeptide (AM466895). The GI peptide contains a tyrosine residue that has not been modified by phosphate or similar charged group. The GI peptide is used to inhibit a signal transduction process that involves binding of a phosphorylated protein or peptide to the SH2 domain of a signal transduction protesh, particularly Grb2. It is used specifically for treatment of hyper-proliferative diseases, especially human cancer
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0
Non-phosphorylated peptide(s) that bind Src Homology 2 domain of signal transducing protein - at least as well as natural phosphorylated target, particularly from treatment of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Non-phosphorylated peptide(s) that bind Src Homology 2 domain of signal transducing protein - at least as well as natural phosphorylated target, particularly from treatment of cancer.
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Pred. No. 0.015;
0; Mismatches 0
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(UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.
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1. .11
                                                                                                                                                                         Disclosure; Page 18; 39pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW46896 standard; peptide; 11 AA.
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100.0%; Pre
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The present sequence represents non-phosphorylated peptide, G1, that is capable of binding to the src homology 2 (SH2) domain of Grb2. Grb2 is a signal transduction protein. The G1 peptide binds to the SH2 domain of Grb2 with affinity similar to, or greater than, that of a SHC grb2 with affinity similar to, or greater than, that of a SHC phosphopeptide (AAW46899). The G1 peptide contains a tyrosine residue that has not been modified by phosphorylate or similar charged group. The G1 peptide is used to inhibit a signal transduction process that involves binding of a phosphorylated protein or peptide to the SH2 domain of a signal transduction protein, particularly Grb2. It is used specifically for treatment of hyper-proliferative diseases, especially human cancer
   Claim 9; Page 17; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11 AA;
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Gaps ·, 97.8%; Score 44; DB 2; Length 11; 100.0%; Pred. No. 0.015; ive 0; Mismatches 0; Indels Ouery Match Best Local Similarity 100...

3 LYENVGMY 10 ത 2 LYENVGMY

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ABG68419 standard; peptide; 11 AA. RESULT 12 ABĢ68419

ABG68419;

(first entry) 07-0CT-2002 31 peptide

Growth factor receptor-bound protein 7; Grb7; ligand; antagonist; cytostatic; cancer; phage display; tumour; metastasis; breast cancer; oesophageal cancer; kidney disorder; liver disorder; gonad disorder; breast disorder; cosophageal disorder; pancreatic disorder; prostate disorder; small intestine disorder; placental disorder; colon disorder; ovary disorder; testicular disorder; lung disorder. 

Synthetic

WO200236142-A2.

05-NOV-2001; 2001WO-US047400.

03-NOV-2000; 2000US-0245755P

(UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE

Krag DN, Pero SC, Oligino L;

WPI; 2002-547451/58

by to Treatment or prophylaxis of a subject having a disorder characterized by abnormal interaction of  $\operatorname{Grb}^7$  and a  $\operatorname{Grb}^7$  ligand, involves administering a non-phosphorylated peptide to a subject in need of the treatment.

Disclosure; Page 102; 186pp; English.

The invention relates to treatment or prophylaxis (M1) of a subject having a disorder characterised by abnormal interaction of Grb7 (Growth factor receptor-bound protein 7 and a Grb7 ligand, comprising administering to a subject in need of the treatment, a non-phosphorylated peptide comprising a sequence (S1, Tyr-Ala-Asn, Tyr-Glu-Asn and Tyr-Asp-Asn) or its functional equivalent, in an amount effective to inhibit the disorder. Also included are peptide antagonists/inhibitors of Grb7, nucleic acids encoding the antagonists, an expression vector comprising the nucleic acid, a host cell transformed or transfected with the vector, screening (M2) a molecular library to identify a compound that inhibits

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interaction between Grb7 and a peptide antagonist and a phage display library comprising Grb7 antagonists. M1 is useful for prophylaxis or treatment of a subject having a disorder characterised by abnormal interaction of Grb7 and a Grb7 ligand, including breast or oesophageal cancer, primary tumour or metastasis, or disorders in kidney, liver, gonads, breast, oesophagus, panoreas, prostate, small intestine, placenta, colon, ovary, testes and lung. The present sequence is a G1 peptide (not defined) or derivative which is used to illustrate the possible structures of cyclic Grb7 antagonists
                                                                                                                                                                                                                                                                                                  Sequence 11 AA;
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. Ouery Match 97.8%; Score 44; DB 5; Length 11; Best Local Similarity 100.0%; Pred. No. 0.015; Matches 8; Conservative 0; Mismatches 0; Indels

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3 LYENVGMY 10 σ 2 LYENVGMY

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; 0

ABG68583 standard; peptide; 11 AA.

RESULT 13

ABG68583;

07-OCT-2002 (first entry)

Peptide GITE #2

Growth factor receptor-bound protein 7; Grb7; ligand; antagonist; cytostatic; cancer; phage display; tumour; metastasis; breast cancer; oseophageal cancer; kidney disorder; liver disorder; gonad disorder; breast disorder; cesophageal disorder; pancreatic disorder; Gl; procate disorder; small intestine disorder; placental disorder; colon disorder; ovary disorder; testicular disorder; lung disorder.

Synthetic

WO200236142-A2.

10-MAY-2002

05-NOV-2001; 2001WO-US047400.

03-NOV-2000; 2000US-0245755P.

(UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.

Oligino L; Krag DN, Pero SC,

by Treatment or prophylaxis of a subject having a disorder characterized b abnormal interaction of Grb7 and a Grb7 ligand, involves administering a non-phosphorylated peptide to a subject in need of the treatment.

Disclosure; Fig 9C; 186pp; English.

The invention relates to treatment or prophylaxis (M1) of a subject having a disorder characterised by abnormal interaction of Grb7 (Growth factor receptor-bound protein 7 and a Grb7 ligand, comprising administering to a subject in need of the treatment, a non-phosphorylated peptide comprising a sequence (S1, Tyr-Ala-Asn, Tyr-Glu-Asn and Tyr-Asp-Asn) or its functional equivalent, in an amount effective to inhibit the disorder. Also included are peptide antagonists/inhibitors of Grb7, nucleic acids encoding the antagonists, an expression vector comprising the nucleic acid, a host cell transformed or transfected with the vector, screening (M2) a molecular library to identify a compound that inhibits interaction between Grb7 and a peptide antagonist and a phage display library comprising Grb7 and a peptide antagonist and a phage display library comprising Grb7 antagonists. M1 is useful for prophylaxis or treatment of a subject having a disorder characterised by abnormal

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RESULT 15
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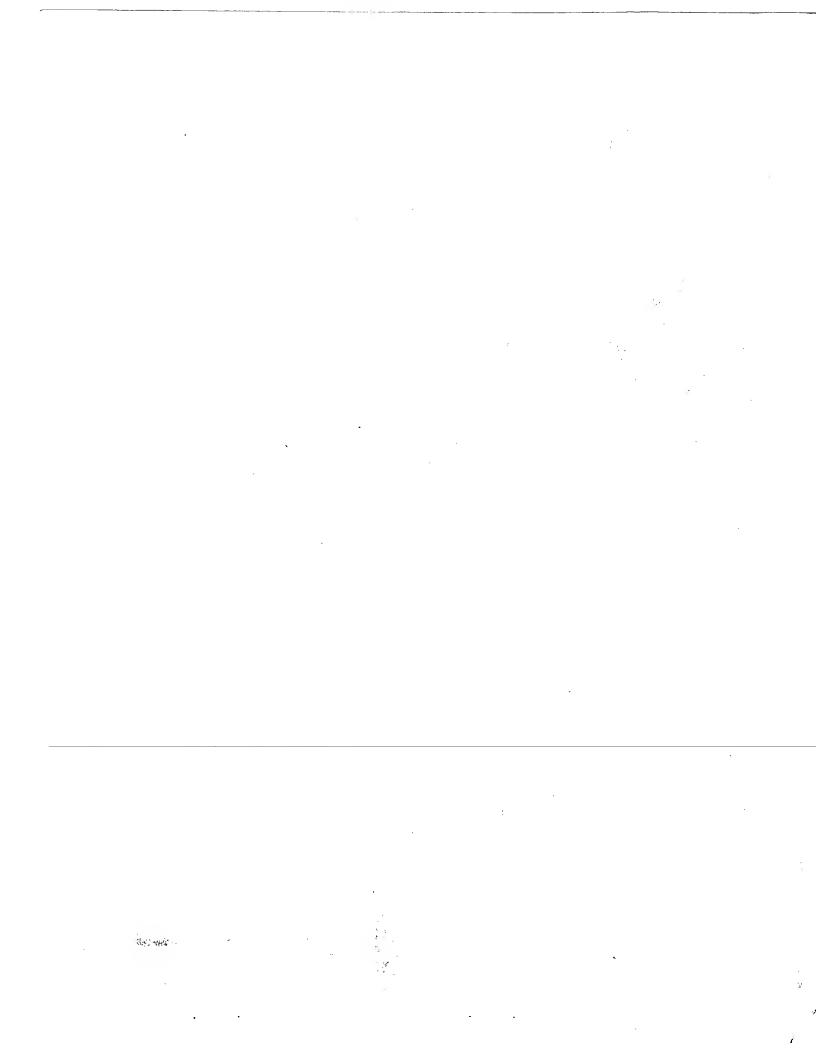
CH2-CHC(O)NH2, where Z is sulphur, sulphoxide, oxygen or methylene, which links the nitrogen atom of the N terminus to the nitrogen acom of the N terminus capacities have a contactor receptor-bound protein 2). On binding Grb2, the peptides have a
                                                                                                                                                                                                                            0
interaction of Grb7 and a Grb7 ligand, including breast or oesophageal cancer, primary tumour or metastasis, or disorders in Kidney, liver, gonads, breast, oesophagus, pancreas, prostatel, small intestine, placenta, colon, ovary, testes and lung. The present sequence is a dipeptide (not defined) or derivative which is used to illustrate the possible structures of cyclic Grb7 antagonists
                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Redox-stable, non-phosphorylated cyclic peptide inhibitors of the Ehmology 2 domain binding to target protein, useful for preventing cancer, especially breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SH2 domain binding inhibitor, non-phosphorylated; redox stable; cytostatic; tumour; breast cancer; linear predursor.
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                                                                                                                                                                                     Length 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acid"
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                                                                                                                                                                                       Score 44; DB 5;
Pred. No. 0.015;
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                                                                                                                                                                     97.8%; Scor.
100.0%; Pred. No. v.
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                                                                                                                                                                                                                                                                                                                                                                                                                   AAB48932 standard; peptide; 26 AA.
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                                                                                                                                                                                                                                     8; Conservative
                                                                                                                                                                                                                                                                                                                 LYENVGMY 10
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                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                  Sequence 11 AA;
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Modified-site
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                                                                                                                                                                                                                                     Matches
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AAB48932
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which bind to Src homology 2 (SH2) domains, preventing them from binding to phosphoryrosine (PTY1) containing regions of target proteins. The cyclic peptides are of one of the following formulae: Xaal-leu2-Tyr3-Glu4-Asn5-Val6-Gly7-Met8-Tyr9-NH or. Xaa2-Leu2-Tyr3-Xaa3-Asn5-Val6-Gly7-Met8-Tyr9-NH or. Xaa2-Leu2-Tyr3-Xaa3-Asn5-Val6-Gly7-Met8-Tyr9-NH where: Xaal is gamma-carboxy-L-glutamic acid (Gla); Xaa2.is 2-aminoadipic acid (Aad, referred to as Adi in the specification); and Xaa3 is either Aad or Glu. Optionally, there is a conservative or neutral amino acid substitution at either or both of Leu2 and Gly7, and optionally one or more of Tyr3, Glu4, Val6, Met8 and Tyr9 is modified. The peptides are cyclised via a bridging moiety of the formula C(0)-CH2-CH2(CHC(0)NH2, where Z is sulphors, sulphoxide, oxygen or methylene, which links the nitrogen atom of the N terminus to the nitrogen atom of
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                                         ø
turn conformation. The peptides, and compositions comprising the peptides, are useful for inhibiting the binding of the SH2 domain to target procein. They are particularly useful for preventing cancer, especially breast cancer. The present sequence represents a linear precursor of a peptide of the invention
                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SH2 domain binding inhibitor; non-phosphorylated; redox stable; cytostatic; tumour; breast cancer; cyclic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SH2 domain cyclic peptide inhibitor, SEQ ID NO:19.
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the C-terminal amide. The peptides are characterised by an in vivo IC-50 cf less than 4.0 micromolar when the target protein is Grb2 (growth factor receptor-bound protein 2). On binding Grb2, the peptides have a turn conformation. The peptides, and compositions comprising the peptides, are useful for inhibiting the binding of the SH2 domain to a target protein. They are particularly useful for preventing cancer, especially breast cancer. The present sequence represents a cyclic peptide of the invention
                                                                                                                                                                                                                                                                                                                                          Gaps
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Search completed: July 20, 2004, 15:43:30 Job time: 53 secs

В 55



us-09-998-350-1, rapb

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66.977 Million cell updates/sec
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6/ptodata/1/pubpaa/USO7 NEW PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Appli	Appli	Appli	Appl:	Appli	App1i	Appli	Appl	Appl	App1	Appl	Appl	Appli	App1i	Appl
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	JS-09-998-3	JS-09-998-3	IE-866-60-SD	US-09-998-3	US-09-998-3	9-99	9-99	9-99	6-6	0-01	6-6	9-99	9-99	9-99	9-99
QI	0-SD	O-SO	O-SO	O-SO	0-SD	O-SD	0-SD	0-SD	us-0	US-1	us-o	0-SD	US-0	ns-o	nS-0
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% Query Match	97.8	97.8	97.8	97.8	97.8	97.8	97.8	97.8	97.8	97.8	97.8	97.8	84.4	84.4	84.4
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## ALIGNMENTS

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RESULT 1
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US-08-150-1
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Sequence 4, Application US/09998350

Sequence 4, Application US/09998350

Sequence 4, Application US/093007836841

Sublication No. US2003007836841

Sublication No. US2003007836841

APPLICANT: Roller P

APPLICANT: Lung, Feng-Di T

APPLICANT: King, Richter C

APPLICANT: King DATE: 2002-12-09

CURRENT APPLICATION NUMBER: PCT/US00/15201

PRIOR FILING DATE: 2000-06-02

PRIOR PPLIANG DATE: 1999-06-02

NUMBER OF SEQ ID NOS: 19

SOFTWARE PATENTIN VINCENDED

SOFTWARE PATENT VINCENDED

SOFTWARE PATENT VINCENDED

SOFTWARE PA
                                                                                   TITLE OF INVENTION: BINDING TO TRREET PROTEIN, CONJUGATES THEREOF, COMPOSITIONS AND NITILE OF INVENTION: BINDING TO TRREET PROTEIN, CONJUGATES THEREOF, COMPOSITIONS AND NITILE OF INVENTION: SYNTHESIS AND USE THIR REPERENCE: 2.14683 CURRENT APPLICATION NUMBER: US/09/998,350 CURRENT FILING DATE: 2002-12-09 PRIOR FILING DATE: 2000-06-02 PRIOR PELICATION NUMBER: PCT/US00/15201 PRIOR FILING DATE: 2000-06-02 PRIOR FILING DATE: 1999-06-02 NUMBER OF SEQ ID NOS: 19 SOFTWARE: PAUGHTING DATE: 1999-06-03 NUMBER: PAUGHTING DATE: 1999-06-02 NUMBER: PAUGHTING DATE: 1999-06-03 NUMBER: PAUGHTING NUMBER: PAUGHTING NUMBER:
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10CATION: (1)...(1)
OTHER INFORMATION: Xaa = Gla, which is gamma-carboxy-L-glutamic acid
FEATURE: INFORMATION: Xaa = Gla, which is gamma-carboxy-L-glutamic acid
MAME/KEY: misc_feature
LOCATION: (1)...(1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Xaa has a ClCH2C(O) - group attached
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Pred. No. 1.2e+06;
0; Mismatches 0;
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100.0%; Pre
0; '
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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OTHER INFORMATION: Synthetic
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
OTHER INFORMATION: Synthetic
FEATURE:
Lung, Feng-Di T
King, Richter C
Yang, Dajun
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 LYENVGMY
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US-09-998-350-4
    APPLICANT:
APPLICANT:
APPLICANT:
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Sequence 3, Application US/0998350
FULICATION NO. US20030078368A1
GENERAL INFORMATION
SAPPLICANT: ROller, Peter P
APPLICANT: Long, Ya-Qiu
APPLICANT: Long, Feng-Di T
APPLICANT: Long, Feng-Di T
APPLICANT: Yang, Bitchter C
APPLICANT: Yang, Bajun
TITLE OF INVENTION: REDOX-STABLE, NON-PHOSPHORYLATED CYCLIC PEPTIDE INHIBITORS OF SH2
TITLE OF INVENTION: BINDING TO TARGET PROTEIN, CONJUGATES THEREOF, COMPOSITIONS AND
TITLE OF INVENTION: SYNTHESIS AND USE
FILE REFERENCE: 214683
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OTHER INFORMATION: Xaa and Tyr at position 9 are bridged together, making this pepti
OTHER INFORMATION: de cyclic
            COATION: (1)..(9)
COTER INFORMATION: Xaa (Gla) and Tyr at position 9 are bridged together, making this
US-09-998-350-1
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LOCATION: (9)._(9)
OTHER INFORMATION: Tyr at position 9 is an amide, i.e., C(O)NH
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97.8%; Score 44; DB 10; L
100.0%; Pred. No. 1.2e+06;
Live 0; Mismatches 0;
                                                                                                                                                                                                       Score 44; DB 10; I
Pred. No. 1.2e+06;
                                                                                                                                                                              97.8%; Scc...
100.0%; Pred. No. 1...
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CURRENT FILING DATE: 2002-12-09
PRIOR APPLICATION NUMBER: COT/US00/15201
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: 60/137,187
PRIOR FILING DATE: 1999-06-02
NUMBER OF SEQ ID NOS: 19
SEQ ID NO 3
SEQ ID NO 3
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; Publication No. US20030078368Al
; GENERAL INFORMATION:
APPLICANT: Roller, Peter P
; APPLICANT: Long, Ya-Qiu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 8; Conservative
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US-09-998-350-7
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Gaps

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APPLICANT: Lung, Feng-Di T
APPLICANT: King, Richter C
APPLICANT: Yours, Day, Daylun
TITLE OF INVENTION: BINDING TO TARGET PROTEIN, CONJUGATES THEREOF, COMPOSITIONS OF SH2
TITLE OF INVENTION: SYNTHESIS AND USE
FILE REPERRNCE: 214683
CURRENT APPLICATION NUMBER: US/09/998,350
CURRENT APPLICATION NUMBER: US/09/998,350
PRIOR RILING DATE: 2002-12-09
PRIOR PAPLICATION NUMBER: 60/137,187
PRIOR FILING DATE: 1999-06-02
NUMBER OF SEQ ID NOS: 19
SEQ ID NO 6
BEOTHER PARTIES ARE PARTIES AND USE
BEOTHER PARTIES AND USE: 1999-06-02
AUGUST AND US BEOTHER PARTIES AND USE: DAYLUS AND AUGUST AND NOS: 19
BEOTHER PARTIES AND USE: 1999-06-02
AUGUST AND NOS: 19
BEOTHER PARTIES AND USE: DAYLUS AND USE AUGUST AND NOS: DAYLUS AND AUGUST AND AUGU
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NAME/KEY: misc feature

OTHER INFORMATION: ic acid

OTHER INFORMATION: ic acid

NAME/KEY: misc_feature

INCATION: (3)...(3)

OTHER INFORMATION: is acid

NAME/KEY: misc_feature

INCATION: (3)...(3)

OTHER INFORMATION: Tyr at position 3 is modified to Tyr(tBu), which is tert-butyl-ty

OTHER INFORMATION: rosine
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LOCATION: (5)...(5)
OTHER INFORMATION: Asn at position 5 is modified to Asn(Trt), which is is trytyl-asp
OTHER INFORMATION: aragine
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NAME/KEY: misc_feature
LOCATION: (9)._(9)
OTHER INFORMATION: Tyr at position 9 is modified to Tyr(tBu), which is tert-butyl-ty
OTHER INFORMATION: rosine
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NAME/KEY: misc_feature

LOCATION: (10)

LOCATION: (10)

OTHER INFORMATION: Cys at position 10 is modified to Cys(Trt), which is trytyl-cyste

OTHER INFORMATION: ine, and Cys(Trt) is connected to a resin

US-09-998-350-6
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Publication No. US20030078368A1
GENERAL INFORMATION:
APPLICANT: Roller, Peter P
APPLICANT: Long, Ya-Qiu
APPLICANT: King, Richter C
APPLICANT: Xing, Richter C
APPLICANT: Yang, Dajun
TITLE OF INVENTION: REDOX-STABLE, NON-PHOSPHORYLATED CYCLIC PEPTIDE INHIBITORS OF SH2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAMM/KEY: misc_feature
LOCATION: (4)...(4)
OTCRE INFORMATION: Glu at position 4 is modified to Glu(OtBu), which is tert-butoxy-
OTHER INFORMATION: glutamic acid
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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Matches 8; Conserv
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LOCATION: (1)...(10)

OTHER INFORMATION: Xaa (Gla) and Cys are bridged together, making this peptide cycli

US-09-998-350-4
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EMBLICATION NO. US20030078368A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Long, Ya-Qiu
APPLICANT: Long, Ya-Qiu
APPLICANT: Long, Reng-Di T
APPLICANT: Yang, Richter C
APPLICANT: Yang, Dajun
TITLE OF INVENTION: REDOX.STABLE, NON-PHOSPHORYLATED CYCLIC FEPTIDE INHIBITORS OF SH2
TITLE OF INVENTION: BINDING TO TARGET PROTEIN, CONJUGATES THEREOF, COMPOSITIONS AND
TITLE OF INVENTION: SYNTHESIS AND USE
FILE REFERENCE: 214693
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                                                                          OTHER INFORMATION: Xaa = Gla, which is gamma-carboxy-L-glutamic acid
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LOCATION: (10) (10)
OTHER INFORMATION: Cys at position 10 is an amide, i.e., C(0)NH
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100.0%; Pred. No. 0.032;
iive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
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CURRENT FILING DATE: 2002-12-09
FRIOR APPLICATION NUMBER: PCT/US00/15201
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: 60/137,187
PRIOR FILING DATE: 1999-06-02
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn version 3.1
SERIOTH: 10
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100.0%;
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 8; Conservative
          NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 LYENVGMY 9
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US-09-998-350-6
                                                 LOCATION:
                                                                                                                                                                                                                                                    FEATURE:
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APPLICANT: Roller, Peter P
APPLICANT: Long, Ya-Qiu
APPLICANT: Long, Ya-Qiu
APPLICANT: Long, Ya-Qiu
APPLICANT: Lung, Feng-Di T
APPLICANT: Lung, Richter C
APPLICANT: King, Richter C
APPLICANT: King, Richter C
APPLICANT: King, Richter C
APPLICANT: Wang John
TITLE OF INVENTION: BINDING TO TARGET PROTEIN, CONJUGATES THEREOF, COMPOSITIONS AND TITLE OF INVENTION: SYNTHESIS AND USE
FILE REFERENCE: 21683
CURRENT APPLICATION NUMBER: PCT/USO0/15201
FRIOR APPLICATION NUMBER: PCT/USO0/15201
PRIOR APPLICATION NUMBER: 60/137,187
PRIOR APPLICATION NUMBER: 1999-06-02
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn version 3.1
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAMB/KEY: misc_feature
LOCATION: (5)._(5)
COTHER INPORMATION: Asn at position 5 is modified to Asn(Trt), which is trityl-aspara
OTHER INFORMATION: gine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (9), [(9) other location of the modified to Tyr(OtBu), which is tert-butoxy-OTHER INFORMATION: tyrosine FEATURE:
                                            NAME/KEY: misc_feature
LOCATION: (1) ...(1)
OCHER INFORMATION: Glu at position 1 is modified to Glu(OtBu), which is tert-butoxy-
OTHER INFORMATION: glutamic acid
                                                                                                                                                                                             FEATURE:
NAME/KEY: misc_feature
LOCATION: (3)._(3)
OTHER INFORMATION: Tyr at position 3 is modified to Tyr(OtBu), which is tert-butoxy-OTHER INFORMATION: tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: (4) ...(4) ...
OTHER INPORMATION: Glu at position 4 is modified to Glu(OtBu), which is tert-butoxy-
OTHER INPORMATION: glutamic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .,
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NAME/KEY: misc_feature
LOCATION: (10)
COTER INFORMATION: Xaa is an amide and is attached to a resin
US-09-998-350-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match

97.8%; Score 44; DB 10; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.032;

Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (10)...(10)
OTHER INFORMATION: Xaa = Nle, which is norleucine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 9
US-09-98-350-14
US-09-988-350-14
Sequence 14, Application US/09998350
Publication No. US20030078368A1
GENERAL INFORMATION
GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
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OTHER INFORMATION: Synthetic
FEATURE:
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US-09-988-350-11

Sequence 11, Application US/09998350

Publication No. US20030078368A1

GENERAL INFORMATION:
APPLICANT: Roller, Peter P
APPLICANT: Long, Ya-Qiu
APPLICANT: Ming, Richter C
APPLICANT: Wang, Dajun
TITLE OF INVENTION: BINDING TO TARGET PROTEIN, CONJUGATES THEREOF, COMPOSITIONS OF SH2
TITLE OF INVENTION: SYNTHESIS AND USE
FILE REFERENCE: 214683

TITLE OF INVENTION: SYNTHESIS AND USE
FILE REFERENCE: 214683

CURRENT APPLICATION NUMBER: DCT/US00/15201

PRIOR APPLICATION NUMBER: 60/137,187

PRIOR PLING DATE: 1999-06-02

PRIOR APPLICATION NUMBER: 60/137,187

PRIOR PLING DATE: 1999-06-02

NUMBER OF SEQ ID NOS: 19

SOFTWARE: Patentin version 3.1

LENGTH: 10
TITLE OF INVENTION: BINDING TO TARGET PROTEIN, CONJUGATES THEREOF, COMPOSITIONS AND TITLE OF INVENTION: SYNTHESIS AND USE FILE REFERENCE: 214683 CURRENT APPLICATION NUMBER: US/09/998,350 CURRENT FILING DATE: 2002-12-09 PRIOR PILING DATE: 2000-06-02 PRIOR PILING DATE: 2000-06-02 PRIOR FILING DATE: 1999-06-02 NUMBER OF SEQ ID NOS: 19 SEQ ID NOS: 19 SEQ ID NOS: 19 SEQ ID NOS: 19 SEQ ID NOS: 10 SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOCATION: (1). (10)
COTHER INFORMATION: Xaa (Adi) and Cys are bridged together, making this peptide cycli
COTHER INFORMATION: c
US-09-998-350-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/EXT: misc_feature
LOCATION: (1). (1)
OTHER INFORMATION: Xaa = Adi, which is alpha-amino-adipic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KER: misc_feature
NAME/KER: misc_feature
OTHER INFORMATION: (1). (1)
OTHER INFORMATION: Xaa has a CH2CO- group attached
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (10) ...(10)
OTHER: INFORMATION: Cys is an amide, i.e., C(0)NH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97.8%; Score 44; DB 10;
100.0%; Pred. No. 0.032;
tive 0; Mismatches
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence FEATURE:
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OTHER INFORMATION: Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Synthetic
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Sequence 18, Application US/09988350
Publication No. US20030078368A1
GENERAL INFORMATION:
APPLICANT: ROller, Peter P
APPLICANT: Loung, Ya-Qiu
APPLICANT: Loung, Feng-Di T
APPLICANT: Ming Richter C
APPLICANT: Wing RICHTER SUBJEC
ATTLE OF INVENTION: BINDING TO TARGET PROTEIN, CONJUGATES THEREOF, COMPOSITIONS AND N
TITLE OF INVENTION: SYNTHESIS AND USE
FILE REFERENCE: 216683
CURRENT APPLICATION NUMBER: US/09/998,350
CURRENT APPLICATION NUMBER: PCT/US00/15201
PRIOR PILING DATE: 2000-06-02
NUMBER OF SEQ ID NOS: 19
SOFTWARE PATENT OF SEQ ID NOS: 19
SOFTWARE PATENT OF SEQ ID NOS: 19
SOFTWARE PATENT OF SEQ ID NOS: 19
SEQ ID NO 18
ENGTH: 26

LENGTH: 26
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Sequence 19, Application US/0998350

Sequence 19, Application US/0998350

GENERAL INFORMATION:

APPLICANT: ROLLE, Peter P

APPLICANT: Long, Ya-Oiu

APPLICANT: Lung, Feng-Di T

APPLICANT: Lung, Feng-Di T

APPLICANT: Lung, Feng-Di T

APPLICANT: Lung, Reicher C

APPLICANT: Lung, Feng-Di T

TITLE OF INVENTION: BINDING TO TARGET PROFEIN, CONJUGATES THEREOF, COMPOSITIONS AND VSE

TITLE OF INVENTION: SYNTHESIS AND USE

TITLE OF INVENTION: SYNTHESIS AND USE

TITLE OF INVENTION: SYNTHESIS AND USE

TITLE OF INVENTION SYNTHESIS AND USE

FILE REFERENCE: 214683

CURRENT FILING DATE: 2002-12-09

PRIOR APPLICATION NUMBER: PCT/US00/15201

PRIOR APPLICATION NUMBER: 60/137,187

PRIOR PILING DATE: 1999-06-02

NUMBER OF SEQ ID NOS: 19

SOFTWARE: PatentIn version 3.1

SEQ ID NO 19

LENGTH: 26
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NAME/KEY: misc_feature
LOCATION: (1) ...(1)
OTHER INFORMATION: Xaa = Gla, which is gamma-carboxy-L-glutamic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature
LOCATION: (1). . (1)
OTHER INFORMATION: Xaa = Gla, which is gamma-carboxy-L-glutamic acid
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100.0%; Pred. No. 0.088;
ive 0; Mismatches 0; Indels
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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OTHER INFORMATION: Synthetic
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Best Local Similarity 100.
Matches 8; Conservative
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US-09-998-350-19
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                                                                                                              PERTURE:
NAME/KEY: misc_feature
LOCATION: (4)...(4)
OCHER INFORMATION: Glu at position 4 is modified to Glu(OtBu), which is tert-butoxy-OTHER INFORMATION: Glutamic acid
FEATURE:
NAME/KEY: misc_feature
LOCATION: (5)...(5)
OCHER INFORMATION: Asn at position 5 is modified to Asn(Trt), which is trytyl-aspara
OCHER INFORMATION: glne
                NAME/KEY: misc_feature
LOCATION: (1)...(1)
OFHER INFORMATION: Glu at position 1 is modified to Glu(OtBu), which is tert-butoxy-
OTHER INFORMATION: glutamic acid
                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAMB/KEY: misc_feature
LOCATION: (9) \( (3) \) (10)
OTHER INFORMATION: Tyr at position 9 is modified to Tyr(OtBu), which is tert-butoxy-
OTHER INFORMATION: tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAMB/KEY: misc_feature
LOCATION: (10) ...(10)
COTHER INFORMATION: Xaa = Adi(OAl), which is allyloxy-alpha-amino-adipic acid
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: No. US20030105000A1-phosphorylated peptide with YEN motif US_10-013-815-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ·.
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APPLICANT: Pero, Stephanie
APPLICANT: Rrag, David
APPLICANT: Rrag, David
TILE APPLICANT: No. Lyn
TILE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING GRB7
FILE REFERENCE: V0139/7048 (HCL/MAT)
CURRENT APPLICATION NUMBER: US/10/013,815
CURRENT APPLICATION NUMBER: US 60/245,755
PRIOR PILING DATE: 2000-11-03
NUMBER OF SEQ ID NOS: 194
SOFTWARE: PatentIn version 3.1
SEQ ID NO 32
LENGTH: 11
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100.0%; Pred. No. 0.035;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97.8%; Score 44; DB 10; Length 10; 100.0%; Pred. No. 0.032; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION: (10) ... (10)
... OTHER THORMATION: Xaa is an amide, i.e., C(O)NH
US-09-996-350-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 32, Application US/10013815; Publication No. US20030105000A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 8; Conservative
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Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
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US-10-013-815-32
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US-09-998-350-18
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US-09-998-350-10
Sequence 10, Application US/09998350
Sequence 10, Application US/09998350
Sequence 10, Application No. US200300783681
GENERAL INFORMATION:
APPLICANT: Roller, Perer P
APPLICANT: King, Richter C
APPLICANT: King, Richter C
APPLICANT: King, Richter C
APPLICANT: Many Peng-Di T
APPLICANT: Many Peng-Di T
APPLICANT: Many Peng-Di T
APPLICANT: Wing, Richter C
APPLICANT: Wi
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. DOCATION: (1).7(10)

. OTHER INFORMATION: Xaa (Adi) at position 1 and Cys are bridged together, making this contex INFORWATION: peptide cyclic US-09-998-350-9
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LOCATION: (1)...(1)
OCHER INFORMATION: At position 1, Xaa = Adi, which is alpha-amino-adipic acid
FEATURE:
NAME/KEY: misc_feature
LOCATION: (4)...(4)
OTHER INFORMATION: At position 4, Xaa = Adi, which is alpha-amino-adipic acid
FEATURE:
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Pred. No. 0.5;
0; Mismatches 1; Indels
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LOCATION: (10) ... (10)
OTHER INFORMATION: Cys is an amide, i.e., C(O)NH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84.4%;
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ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: Synthetic
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Best Local Similarity 87.5
Matches 7; Conservative
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Publication No. US2003007836841

GENERAL INFORMATION

APPLICANT: Roller, Peter P

APPLICANT: Lung, Ya-Qiu

APPLICANT: Lung, Reng-Di T

APPLICANT: Lung, Reng-Di T

APPLICANT: VARION REDOX-STABLE, NON-PHOSPHORYLATED CYCLIC PEPTIDE INHIBITORS OF SH2

TITLE OF INVENTION: BINDING TO TARGET PROTEIN, CONJUGATES THEREOF, COMPOSITIONS AND

TITLE OF INVENTION: BINDING TO TARGET PROTEIN, CONJUGATES THEREOF, COMPOSITIONS AND

TITLE OF INVENTION: BINDING TO 128.09/998,350

CURRENT APPLICATION NUMBER: US/09/998,350

CURRENT APPLICATION NUMBER: PCT/US00/15201

PRIOR APPLICATION NUMBER: 60/137,187

PRIOR APPLICATION NUMBER: 60/137,187

PRIOR FILING DATE: 1999-06-02

NUMBER OF SEQ ID NOS: 19

SOFTWARE: Patentin Version 3.1

SEQ ID NO 2
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LOCATION: (1). 7(1)
OTHER INFORMATION: Xaa at position 1 is alpha-amino-adipic acid (Adi)
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                                     NAME/KEY: misc_feature
LOCATION: (1)._(1)
OTHER INFORMATION: Xaa (Gla) has a CH2CO- group attached
                                                                                                                                                                  PEATURE:

NAME/KEY: misc_feature

LOCATION: (10)

. OTHER INPORMATION: Cys is an amide, i.e., C(O)NH
US-09-998-150-19
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Best Local Similarity 87.5%; Pred. No. 1.2e+06;
Matches 7; Conservative 0; Mismatches 1.
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LOCATION: (4). 7(4)
OTHER INFORMATION: Xaa at position 4 is Glu or
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ORGANISM: Artificial Sequence
FEATURE:
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NAME/KEY: misc_feature
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US-09-998-350-2
FEATURE:
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PRIOR APPLICATION NUMBER: PCT/USO0/15201

PRIOR FILING DATE: 2000-06-02

PRIOR FILING DATE: 1990-06-02

PRIOR FILING DATE: 1999-06-02

NUMBER OF SEQ ID NOS: 19

SCOTTANE: PREDICT VERSION 3.1

LENGTH: 10

TYPE: PRI

ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Synthetic

FRATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(1)

OTHER INFORMATION: Glu has a CH2CO- group attached

FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(1)

OTHER INFORMATION: Xaa = Nle, which is norleucine

FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(10)

OTHER INFORMATION: Glu and Cys are bridged together, making this peptide cyclic

US-09-998-350-10
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84.4%; Score 38; DB 10; Length 10;

Best Local Similarity 87.5%; Pred. No. 0.5;

Matches 7; Conservative 0; Mismatches 1; Indels
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Search completed: July 20, 2004, 15:46:30 Job time : 42 secs

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GenCore version 5.1.6

Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 20, 2004, 15:32:08 ; Search time 13 Seconds

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36.049 Million cell updates/sec
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Title: US-09-998-350-1 Perfect score: 45 Sequence: 1 XLYENVGMY 9

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 141681 segs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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## ALIGNMENTS

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Usage

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modified and this statement is not removed.
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Best Local Similarity 75.0
Matches 6; Conservative
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VGLG_SIGMA
ID _VGLG_SIGMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Res. Virol. 145:25-35(1994).
-!- FUNCTION: This protein is one of the structural proteins in the viral coat and is synthesized during late infection.
-!- SUBUNIT: Homotrimer (By similarity).
                                                                                          EMBL; X03183; CA26944.1; ---
R. EMBL; M1578; AA34875.1; ---
R. EMBL; M1578; AA34875.1; ---
R. EMBL; Z75294; CAA99718.1; ---
R. EMBL; Z75294; CAA99718.1; ---
R. ESP; PO0914; 1DNP.
R. Germonline; 143974; ---
R. Germonline; 143974; ---
R. Germonline; 143974; ---
R. InterPro; IPR002081; DNA_photolysse_1.
R. InterPro; IPR006301; FAD_binding_7.
R. InterPro; IPR006501; FAD_binding_7.
R. RP00875; DNA_photolysse_1.
R. PF00441; FAD_binding_7.
R. PRNNS; PR00147; DNAPHOTUKÄSE.
R. PRODGH; PO004399; DNA_PHOTOLYÄSES 1.1; 1.
R. PROSTTE; PS00691; DNA_PHOTOLYÄSES 1.1; 1.
W. Muclear protein; Mitochondrion; Transit peptide.
TRANSIT
TRANSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human adenovirus type 31.
Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
NCBI_TaxID=10529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=WRL 15/62;
PUDMed=8023012;
Pring-Akerblom P., Adrian T.;
"Type- and group-specific polymerase chain reaction for adenovirus detection.";
Refection.";
Res. Virol. 145:25-35(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEOXYRIBODIPYRIMIDINE PHOTOLYASE.
H-T-H MOTIF (POTENTIAL).
V -> A (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | Length 565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRC64;
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S -> S (IN REF. 2).
S -> T (IN REF. 2).
S -> T (IN REF. 2).
S -> R (IN REF. 2).
G -> E (IN REF. 2).
C -> E (IN REF. 2).
C -> E (IN REF. 2).
C -> C (IN REF. 2).
C -> C (IN REF. 2).
C -> C (IN REF. 2).
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Pred. No. 3;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
10-BC-1998 (Rel. 37, Last annotation update)
Hexon protein (Late protein 2) (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66274 MW;
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Best Local Similarity 75.0
... 6; Conservative
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87 LYDNVGLY 94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               265
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HEX ADE31

AC P36855;
DT O1-UNW-1994
DT O1-UWW-1994
DT 15-DEC-1998
DE HEXON PICLE
GN Human adenc
OC VITUSES; ds
OC VITUSES; ds
OC NCEL TAXID-
RN [1]
RN ENDLINE-942
RX MEDLINE-942
RX MEDLINE-94
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CONFLICT
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CONFLICT
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(See http://www.isb-sib.ch/announce/
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32 N-LINKED (GLCNAC. .) (POTENTIAL)
445 N-LINKED (GLCNAC. .) (POTENTIAL)
59010 MM; 335607C69249DD9D CRC64;
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Teninges D., Bras-Herreng F.;
"Rhabdovirus sigma, the hereditary CO2 sensitivity agent of
Drosophila: nucleotide sequence of a cDNA clone encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                     Score 36; DB 1; Length 468;
Pred. No. 6.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 36; DB 1; Length 526;
Pred. No. 7.3;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Viruses, ssRNA negative-strand viruses, Mononegavirales,
Rhabdoviridae, unclassified Rhabdoviridae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FITY Asse; FERONO15809; sigma-Virus\G.
InterPro; IPRO01903; Rhabd_glycop.
Pfam; PF00974; Rhabdo glycop. 1.
Pransmembrane; Envelope protein; Glycoprotein; Signal.
SIGNAL 1 17 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                     468 AA; 52100 MW; 8727BFA49179CE68 CRC64;
                                                                          EMBL, X74661, CAA55725.1; -. PIR, S37217, S37217.
HSSP, P03277; 1DHX.
Interpro; IPR000736; Adeno hexon.
Pfam; PF01065; Adeno hexon; 1.
ProDom, PD02815; Adeno hexon; 1.
Coat protein; Hexon protein; Late protein.
NON TER 468 468
SEQÜENCE 468 AA; 52100 MW; 8727BFA49179CE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P12647;
01-0CT-1989 (Rel. 12, Created)
28-CTE-2093 (Rel. 12, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Spike glycoprotein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    526 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
   entities requires.a license agreement (@ or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        glycoprotein.";
J. Gen. Virol. 68:2625-2638(1987)
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HEX\_ADE12 P19900;

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                                                                                                                         X MEDLINE-129947; PubMed=2034671;
X MEDLINE-1299677; PubMed=2034671;
A Rammerloher W., Obermaier-Skrobranek B.M.M., Estermaier L.M.,
A Rammerloher W., Freund C., Wuelfing C., Burkert U.I., Matern D.H.,
A Breuer M., Edit Z.M., Kuefrevioglu O.I., Hartmann G.R.,
I "Isolation and properties of a nitrile hydratase from the soil fungus
Myrothecium verrucaria that is highly specific for the fertilizer
T cyanamide and cloning of its gene.",
Proc. Natl. Acad. Sci. U.S.A. 88:4260-4264(1991)
L. Proc. Natl. Acad. Sci. U.S.A. 88:4260-4264(1991)
C. --- PUNCTION: When used as herbicide in agriculture, cyanamide can be transformed, after sowing, in soil fertilizing ammonia by the combined action of M.verrucaria cyanamide hydratase and urease.
C. --- COFACTOR: Zinc.
C.-- COFACTOR: Zinc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PERMINE SOLAGE RO-67;

MEDLINE=95407102; PubMed=7676636;

Pring=Akerblom P., Trijssenaar J., Adrian T.;

Pring=Akerblom P., Trijssenaar J., Adrian T.;

Pring=Akerblom P., Trijssenaar J., Adrian T.;

Sequence characterization and comparison of human adenovirus subgenus B and E hexons.";

Virology 212:232-236 (1995).

-1. FUNCTION: This protein is one of the structural proteins in the viral coat and is synthesized during late infection.

-1. SUBUNIT: Homotrimer (By similarity).
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae, Hypocreales; mitosporic Hypocreales; Myrothecium.
NCBI_TaxID=5532;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human adenovirus type 4.
Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           - SUBUNIT: Homohexamer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77.8%; Score 35; DB 1; Length 244; 75.0%; Pred. No. 5.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           244 AA; 26966 MW; 880FAllF30E31CE2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-UUN-1994 (Rel. 29, Created)
01-UUN-1994 (Rel. 29, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hexon protein (Late protein 2) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          447 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                               SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A39365; A39365.
InterPro; IPR006674; HD.
InterPro; IPR003607; Met_phsphohydro.
Pfam, PF01966; HD; 1.
PRART; SM00471; HDc; 1.
Lyase; Zinc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M59078; AAA33429.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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P36850;
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HEX_ADE04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The primary structure of human adenovirus type 12 protease.";
Nucleic Acids Res. 16.7195-7195(1988).
-!- FUNCTION: This protein is one of the structural proteins in the viral coat and is synthesized during late infection.
-!- SUBUNIT: Homotrimer (By similarity).
                                                                                                                                                                                                                                                                                                 Human adenovirus type 12.
Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

MEDLINES-84076430; PubMed=8254750;
Sprengel J., Schmitz B., Heuss-Neitzel D., Zock C., Doerfler W.;
"Nucleotide sequence of human adenovirus type 12 DNA: comparative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ·,
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EMBL, X07655; CAA30501.1; -...
EMBL, X07655; CAA3192.1; -...
EMBL, X07655; CAB3192.1; -...
EMBL, X01730; S01730.
PIR, S01730; S01730.
PIR, S01770; DHX.
InterPro; IPR000736; Adeno_hexon.
Fram; PF01065; Adeno_hexon, 1...
Fram; PF01065; Adeno_hexon C: 1...
Fram; PF02678; Adeno_hexon C: 1...
ProDom; PD0022815, Adeno_hexon, 1...
Coat protein; Hexon protein; Late protein.
SEQUENCE 919 AA; 103039 MW; B37167885A516288 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80.0%; Score 36; DB 1; Length 919; 75.0%; Pred. No. 13; ive 1; Mismatches 1; Indels
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01-AUG-1991 (Rel. 19, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
CAH.
                                                                                                                                                                             01-FEB-1991 (Rel. 17, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=88303354; PubMed=3043380;
Weber J.M., Houde A.;
                                                                                                                                                                                                                                                         Hexon protein (Late protein 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 888-919 FROM N.A. STRAIN=Pereira 1131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            functional analysis.";
J. Virol. 68:379-389(1994).
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                                                                                                                                   STANDARD;
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                 351 LYQSVGMY 358
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HEX ADER 12

HEX ADER 12

DT 01-FE DT 0

CYAH MYRVE P22143;

RESULT 5

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CYAH MYRVE
ID CYAH MA
AC P2143;
AC 01-40GDT 01-AUGDT 15-JULDE Cyanami
OS Myrothe

Query Match

Matches

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Gaps

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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -! - FUNCTION: Hemagglutinin is responsible for attaching the virus to cell receptors and for initiating infection.
-!- SUBUNIT: Homotrimer. Each of the monomers is formed by two chains (HA1 and HA2) linked by a disulfide bond.
-!- SIMILARITY: Belongs to the influenza viruses hemagglutinin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-81030852; PubMed=7421990;
Gething M.-J., Bye J., Skehel J.J., Waterfield M.;
"Cloning and DNA sequence of double-stranded copies of haemagglutinin genes from H2 and H3 strains elucidates antigenic shift and drift in human influenza virus.";
Nature 287:301-306(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hemagglutinin Precursor [Contains: Hemagglutinin HAl chain;
                                                                                                                                                                                                                                                                                                                                                                                                                        77.8%; Score 35; DB 1; Length 447; 75.0%; Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Influenza A virus (strain A/Japan/305/57).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza A viruses; Influenzavirus A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HESEP, P00437, 1HTM.

InterPro; IPR008980; Capsid hemag.

InterPro; IPR001364; Hemagglutin.

PRINTS; PR00329; Hemagglutinin; 1.

PRINTS; PR00325; Hemagglutini; 1.

Brobom; PD000225; Hemagglutini; 1.

Envelope protein; Hemagglutinii; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                        447 447
447 AA; 49553 MW; A7AE1977F707BD4D CRC64;
                                                                                                                                                                                                                                                                                                    Coat protein; Hexon protein; Late protein.

NON TER 447 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                   PIR; S39296; S39296.
HSSP; P03277; DDHX.
InterPro: IPR000736; Adeno hexon.
Pfam; PF01065; Adeno hexon; 1.
ProDom; PD002815; Adeno hexon; 1.
                                                                                                                                                               EMBL; X76550; CAA54052.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; J02127; AAA43185.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 75.0
les 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  356 LYANVGLY 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 LYENVGMY 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A04062; HMIV2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=11421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HEMA IAJAP
P03451;
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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HENA IAJAP
HENA IAJAP
HON HASSIL
DT 21-UJU.
DT 21-UJU.
DT 10-OCT.
DE Hemagg.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: Contains 1 GTPase-binding (GBD) domain.
-!- SIMILARITY: Contains 1 Formin homology 1 (FH1) domain.
-!- SIMILARITY: Contains 1 Formin homology 2 (FH2) domain.
-!- SIMILARITY: Contains 1 Formin homology 3 (FH3) domain.
-!- SIMILARITY: Contains 1 DRF autoregulatory (DAD) domain.
-!- SIMILARITY: Belongs to the formin homology family. Diaphanous
                                                                                                                                                                                                                                                                                                                                                                                                                                          DIA2_HUMAN STANDARD; PRT; 1101 AA.
060879, 050878, 050478, 050478, 11012.
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-JUL-1999 (Rel. 38, Last sequence update)
16-JUL-1007-2003 (Rel. 42, Last annotation update)
Diaphanous protein homolog 2 (Diaphanous-related formin 2) (DRF2)
DIAPH2 OR DIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Homo.
                                                                       GLCNAC...) (POTENTIAL).
GLCNAC...) (POTENTIAL).
GLCNAC...) (POTENTIAL).
GLCNAC...) (POTENTIAL).
GLCNAC...) (POTENTIAL).
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S
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Borsani G., Jonveaux P., Philippe C., Zuccotti M., Ballabio A.,
Toniolo D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (by similarity).
-!- DISBASE: Defects in DIAPH2 are a cause of premature ovarian failure (POF) [MIM:311360].
                                                                                                                                                                                                                                                                     ;
0
                                      (POTENTIAL)
                                                                                                                                                                                                                           77.8%; Score 35; DB 1; Length 562; 75.0%; Pred. No. 13; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Heath P.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: May be involved in oogenesis.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                          6B7FD0C038993630 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Event=Alternative splicing; Named isoforms=2;
                                N-LINKED (GLCNAC
HEMAGGLUTININ HAI
HEMAGGLUTININ HAZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
MEDLINE=98163437; Pubmed=9497258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=DIA-156;
IsoId=O60879-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Am. J. Hūm. Genet. 62:533-541(1998).
[2]
                                                                                                                                                                                          63118 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 685-906 FROM N.A.
                                                                                                                                                                                                                                                                     Conservative
||:|||
204 LYONVGTY 211
                                                                                                                                                                                                          Query Match
Best Local Similarity
6, Conserve
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2 LYENVGMY 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=DIA-12C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    subfamily
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CARBOHYD CARBOHYD
                                                                                           CARBOHYD
CARBOHYD
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CARBOHYD
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Bristol N2;
MEDLINE=94150718; PubMed=7906398;
Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   399F1C292D79188B CRC64;
                                                                                                                                                                                                                                                                                                                                                                         COILED COIL (POTENTIAL)
COILED COIL (POTENTIAL)
FH1 (PRO-RICH).
                                                                                                                                                                                                                                                                                                                                                                                                                         FH2.
COILED COIL (POTENTIAL)
                                                                                                                       EMBL; Y15909; CAA75870.1;
EMBL; Y15909; CAA75870.1;
EMBL; Y15909; CAA75870.1;
EMBL; AL031033; CAA39108.1;
EMBL; AL031033; CAA39108.1;
EMBL; AL031035; CAA39108.1;
EMBL; AL03104; Execeptor binding; TAS.
MIM; 310360; ----
EGO; GO:0005102; F:receptor binding; TAS.
GO; GO:000529; P:female gamete generation; TAS.
InterPro; IPRO3104; FRZ.
EGO; GO:000529; P:female gamete generation; TAS.
InterPro; IPRO4104; FRZ.
EGO; GO:000599; FRZ; 1.

Alternative splicing; Coiled coil; Repeat.
EGOMAIN 184 482 FH3:
EGOMAIN 366 418 COILED COIL (POTENTIAL DOWAIN 487 547 COILED COIL (POTENTIAL DOWAIN 549 623 FH1 (PRO-RICH).
EGOMAIN 1054 1068 DAD.
EGOMAIN 1054 1068 DAD.
EGOMAIN 1072 1075 ARG/LYS-RICH (BASIC).
EGOMAIN 543 546 POLY-ERD.
EGOMAIN 550 572 POLY-PRO.
EGOMAIN 576 585 POLY-PRO.
EGOMAIN 576 585 POLY-PRO.
EGOMAIN 576 585 POLY-PRO.
EGOMAIN 576 585 POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DIA-12C).
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ARG/LYS-RICH (BASIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
FEB-2003 (Rel. 41, Last annotation update)
Hypothetical protein F22B7.3 in chromosome III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     001573
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75.6%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 75...
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               971 LYENLGEY 978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 LYENVGMY 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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28-FEB-2003 (Rel. 41, Last annotation update)
Formate dehydrogenase, iron-sulfur subunit (Formate dehydrogenase beta subunit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: ALLOWER TO USE FORMATE AS MAJOR ELECTRON DONOR DURING ANAEROBIC RESPIRATION. THE BETA CHAIN IS AN ELECTRON TRANSFER UNIT CONTAINING 4 CYSTEINE CLUSTERS INVOLVED IN THE FORMATION OF IRON-SULFUR CENTRES. ELECTRONS ARE TRANSFERRED FROM THE GAMMA CHAIN TO THE MOLYBDENUM COPACTOR OF THE ALPHA SUBUNIT (BY SIMILARITY). SUBUNIT: FORMATE DEHYDROGRASE IS A MEMBRANE BOUND COMPLEX, FORMED BY SUBUNITS ALPHA, BETA AND GAMMA.

SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: ORTHOLOG OF BOTH E.COLI FDNH AND FDOH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                            æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Rd / KW20 / ATCC 51907;
STRAIN=Rd / KW20 / ATCC 51907;
MEDLINE=95250630; PubMed=7542800;
Pleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
McKenney K., Sutton G., Fitzhngh W., Fields C.A., Gocayne J.D.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Riffor L., Roopra A., Saunders D., Shownkeen I
Sims M., Smaldon N., Smith A., Smith M., Sonnhammer B., Staden R.,
Sulston J., Thierry-Meg J., Thomas K., Vaudin M., Vaughan K.,
Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
                                                                                                                                                   12.2 Mb of contiguous nucleotide sequence from chromosome III of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria, Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 33; DB 1; Length 99;
Pred. No. 5.4;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11665 MW; 78FC94DBD3C8B585 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           312 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 71.4%;
nes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, L12018; AAA65463.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; S44632; S44632.
WormPep; F22B7.3; CE00156.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 269:496-512(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                         Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 YENVGMY 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99 AA;
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ID FDXH HAEIN
AC P44450;
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Best Local S:
Matches 5,
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=89232744; PubMed=3073107;
Gietz R.D., Prakash S.j.
"Cloning and nucleosic sequence analysis of the Saccharomyces "Cloning and nucleose sequence for excision repair of UV-damaged cerevisiae RAD4 gene required for excision repair of UV-damaged
                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                          Length 312;
                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                  HSSP; P00193; IDUR.
TIGR, H10007; IDUR.
TIGR, H10007; IDUR.
TIGRAM: PR00450; FDH_beta.
InterPro: IRR06470; FDH_beta.
TIGRAMS; TIGR01582; FDH_beta; 1.
TIGRAMS; TIGR01582; FDH_beta; 1.
Electron transport; 4Fe4S_FERREDOXIN; 1.
Complete proteome.
                                                                                                                                                                                        CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccha
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                       (4FE-4S)
                                                                                                                                                                                                                                                                                           (4FE-4S)
                                                                                                                                                                                                                                                                                                                       (4FE-4S)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-89197751; PubMed=2649477;
Couto L.B., Friedberg B.C.;
"Nucleotide sequence of the wild-type RAD4 gene
                                                                                                                                                                                                                                                                                                                                          AA49DD3C17064866
                                                                                                                                                                                                                                                                                                                                                           73.3%; Score 33; DB 1; 71.4%; Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
10-0cT-2003 (Rel. 42, Last annotation update)
DNA repair protein RAD4.
                                                                                                                                                                                               IRON-SULFUR 1
IRON-SULFUR 1
IRON-SULFUR 1
IRON-SULFUR 2
IRON-SULFUR 2
IRON-SULFUR 2
IRON-SULFUR 3
IRON-SULFUR 4
                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                        IRON-SULFUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                          34068 MW;
                                                                                  EMBL; U32686; AAC21685.1; -. PIR; A64042; A64042.
                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 71.4 (es 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene 74:535-541(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                   214 YENAGLY 220
                                                                                                                                                                                                                                                                                                                                         312 AA;
                                                                                                                                                                                                                                                                                                                                                                                                3 YENVGMY 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4932;
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P14736;
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SEQUENCE
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                                                                                     SEQUENCE FROM N.A.

SERAINS=S286C, AB972;

STRAINS=S286C, DubMed=9169868;

Dictrich F.S., Mulligan J.T., Hennessy K.M., Yelton M.A., Allen E.,

Araujo R., Aviles E., Berno A., Brennan T., Carpenter J., Chen E.,

Cherry J.M., Chung E., Duncan M., Guzman E., Hartzell G.,

Hunicke-Smith S., Hyman R.W., Kayser A., Komp C., Lashkari D., Lew H.,

Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P.,

Oh C., Petel F.X., Roberts D., Schl P., Schramm S., Shogren T.,

Smith V., Taylor P., Wei Y., Botstein D., Davis R.W.;

"The nucleotide sequence of Saccharomyces cerevisiae chromosome V.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 387:76-81(1997).
-!- FUNCTION: Involved in nucleotide excision repair of DNA damaged with UV light, bulk adducts, or cross-linking agents.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: Belongs to the XPC family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0000111; C:nucleotide excision repair factor 2 complex, IDA.
GO; GO:000108; C:repairosome; IDA.
GO; GO:0003684; F:damaged DNA binding; IDA.
Interpro. IPRO04583; Rad4.
TIGRFAMS; TIGR00605; rad4; 1.
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STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
MEDLINE=96337999; PubMed=8688087;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 754;
cerevisiae and characterization of mutant rad4 alleles.";
J. Bacteriol, 171:1862-1869(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
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VGI -> EGL (IN REF. 3).
788C146DC4BD2BF8 CRC64;
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15-UUL-1998 (Rel. 36, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Aspartate carbamoyltransferase (BC 2.1.3.2) (Aspartate transcarbamylase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Archaea; Euryarchaeota; Methanococci; Methanococcales; Methanocaldococcaceae; Methanocaldococcus.
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Pred. No. 45;
2; Mismatches
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DNA_BIND 250 269 POTENTIAL.
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EMBL, M24928; AAA34945.1; --
EMBL, U18917, AAB64669.1; --
PIR, S30814; DDBYD4.
GermOnline; 139239; --
SGD; S0000964; RAD4.
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754 AA; 87174 MW;
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71.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              220 YDNVGIY 226
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=2190;
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ID PYRB METJA
AC Q58976;
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SECUENCE FROM N.A., AND MUTAGENESIS OF ARG-15.
STRAIN=K1-23; TRANSPOSON=Th5306;
MEDLINE=55263576; PubMed=7744873;
Donkersloot J.A., Thompson J.;
"Cloning, expression, sequence analysis, and site-directed mutagenesis of the Tm5306-encoded N5-(carboxyethyl)ornithine synthase from Lactococcus lactis Kl."
J. Biol. Chem. 270:12226-12234 (1995).
                                                                  Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
                                                                                                                                                                                                                                                                                                                          Thompson J.; "N5-(L-1-carboxyethyl)-L-ornithine:NADP+ oxidoreductase from Streptococcus lactis. Purification and partial characterization."; J. Biol. Chem. 264:9592-9601(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=K1;
MEDLINE=20014035; PubMed=10548058;
Sacket D.L., Ruvinov S.B., Thompson J.;
NS-(L-1-carboxyethyl)-L-ornithine synthase: physical and spectral characterization of the enzyme and its unusual low pKa fluorescent tyrosine residues.";
   28-FEB-2003 (Rel. 41, Last annotation update)
N(5)-(carboxyethyl)ornithine synthase (EC 1.5.1.24) (N(5)-(L-1-carboxyethyl)-L-ornithine:NADP(+) oxidoreductase) (CEOS).
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 256-263, AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99456521; PubMed=10525296;
                                                                                                                                                                                                                                                                                            STRAIN=K1;
MEDLINE=89255467; PubMed=2498334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein Sci. 8:2121-2129(1999)
                                                                                                                                                                                                                                                                              SEQUENCE OF 1-37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FOLDING STUDIES.
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O
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D., Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reith C.I., Soverbeek R., Kirkness E.F., Weinstoock K.G., Merrick J.M., Glodek A., Scott J.L., Geoghagen N.S.M., Weidman J.E., Fuhrmann J.L., Nguyen D., Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Veneer J.C., "Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                    + N-carbamoyl-L-aspartate.
-!- PATHWAY: Pythindine biosynthesis, second step.
-!- SPATHWAY: Pythindine biosynthesis; second step.
-!- SUBUNIT: HETERODOBEAMER (23:3R2) OF SIX CATALYTIC PYRB CHAINS ORGANIZED AS TWO TRIMERS (C3), AND SIX REGULATORY PYRI CHAINS ORGANIZED AS THREE DIMERS (R2).
-!- SIMILARITY: Belongs to the ATCase/OTCase family.
                                                                                                                                                                                                           Hack E.S., Vorobyova T., Sakash J.B., West J.M., Macol C.P., Herve Williams M.K., Kantrowitz E.R., Characterization of the aspartate transcarbamoylase from Merhanocoms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71.1%; Score 32; DB 1; Length 306; 75.0%; Pred. No. 29; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIGREAMS; TIGRO0670; asp carb tr; 1.
PROSITE; PS00097; CARBAMOYLTRĀNSFERASE; 1.
Pyrimidine biosynthesis; Transferase; Complete proteome.
SEQUENCE 306 AA; 35159 MW; CBDC31FC450CEF6A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HAMAS, ME_00001; -; 1.
InterPro; IRR065130; Asp/orn Cotranf.
InterPro; IRR0065130; Asp_carEmitransf.
InterPro; IRR006131; OTCace O.
InterPro; IRR006132; OTCace P.
Pfam; PR00185; OTCace; 1.
Pfam; PR00185; OTCace N; 1.
Pfam; PR02729; OTCace N; 1.
                                                                                                                                                                                                                                                          Methanococcus jannaschii.";
J. Biol. Chem. 275:15820-15827(2000).
                                                                                                                                                                            CHARACTERIZATION.
MEDLINE=20283607; PubMed=10748118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U67598; AAB99601.1; -. PIR; D64497; D64497; ASSU. TIGR; MJ1581; -.
                                                                                                                                            Science 273:1058-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 75.0
                                                                                                                               annasch11
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Ruvinov S.B., Thompson J., Sackett D.L., Ginsburg A.,
"Tetrameric N(5)-(L-1-carboxyethyl)-L-ornithine synthase: guanidine.
HOL-induced unfolding and a low temperature requirement for
refolding.";
Arch. Biochem. Biophys. 371:115-123(1999).
-! GYTALYTIC ACTIVITY: N(5)-(L-1-carboxyethyl)-L-ornithine + NADP(+)
-! GYTALYTIC ACTIVITY: N(5)-(L-1-carboxyethyl)-L-ornithine + NADP(+)
-! SUBUNIT: Homotetramer.
-! MASS SPECTROMETRY: MW=35.355; METHOD=MALDI.
-! MASS SPECTROMETRY: MW=35.355; METHOD=MALDI.
-! GIL-ornithine, more slowly, yielding N(6)-(L-1-carboxyethyl)-L-
lysine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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INTERPO; IPR007698; AlaDh PNT C.
INTERPO; IPR007086; AlaDh PNT N.
Pfam; PF05222; AlaDh PNT N; 1.
Oxidoreductase; NAPP.
NP BIND 171 176 NADPH (POTENTIAL).
NP BIND 15 15 R->K; LOSS OF ACTIVITY.
SEQUENCE 313 AA; 35323 NW; B17FE0F477113C77 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71.1%; Score 32; DB 1; 62.5%; Pred. No. 29; ive 1; Mismatches
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Best Local Similarity
Matches 5; Conservat
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Gaps

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RESULT 13
CED2\_LACLA
TD CED2\_LACLA
STANDARD; PRT; 313 AA
AC P15244;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)

LFENVEMY 182 LYENVGMY 9

N 175

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Garcia J.L., Diaz E.;
"Catabolism of phenylacetic acid in Escherichia coli. Characterization of a new aerobic hybrid pathway.";
J. Biol. Chem. 273:25974-25986 (1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             catabolic operons for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHENYLACETYL-COA.
-!- CATALYTIC ACTIVITY: ATP + phenylacetate + CoA = AMP + diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDIINES 97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III; Bloch C.A., Perna N.T., Burland V.,
Blattner F.R., Plunkett G. III; Bloch C.A., Rode C.K., Mayhew G.F.,
Criado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ferrandez A., Minambres B., García B., Olivera E.R., Luengo J.M.,
García J.L., Diaz E.;
                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                              (Phenylacetyl-CoA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20229831; PubMed=10766858; Ferrandez A., Garcia J.L., Diaz E.; "Transcriptional regulation of the divergent paa catabolic oper phenylacetic acid degradation in Escherichia coli."; J. Biol. Chem. 275:12214-12222(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         + phenylacetyl-CoA.
--- PATHWAX: Phenylacetic acid aerobic catabolism; first step.
--- INDUCTION: Aciivated by CAMP receptor protein (CRP) and integration host factor (IHF). Inhibited by paax.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 32; DB 1; Length 437; Pred. No. 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., SEQUENCE OF 1-6, AND CHARACTERIZATION STRAIN=W / ATCC 11105;
MEDLINE=98421522; PubMed=9748275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -> T (IN STRAIN W).
3D49DB382B80F98A CRC64;
                                                                                                                                                                                         Proms; 053018; 16-007-2001 (Rel. 40, Created) 16-007-2001 (Rel. 40, Last sequence update) 16-007-2001 (Rel. 40, Last amontation update) Phenylacetate-coenzyme, A ligase (EC 6.2.1.30)
                                                                                                                                                                          437 AA
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EMBL; AE000236; AAC74480.1; -.
PIR; A64891; A64891.
                                                                                                                                                                    PRT;
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InterPro; IPR000873; AMP-bind.
Pfam; PF00501; AMP-binding; 2.
Ligase; Complete proteome.
VARIANT 127 S-
SEQUENCE 437 AA; 48952 MW; 3
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85.7%;
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                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                             ligase) (PA-CoA ligase)
PAAK OR B1398.
                                                262 IYENAGKY 269
     2 LYENVGMY 9
                                                                                                                                                                                                                                                                                                                                                                        Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=562;
                                                                                                                                                                            PAAK ECOLI
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Best Local Similarity

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINES-91124738; PubMed=1733105;
MCSEG M.A., MARKIOLL A.C., Nuttall P.A.;
Morse M.A., MARKIOLL A.C., Nuttall P.A.;
"The glycoprotein of Thogoto virus (a tick-borne orthomyxo-like virus) is related to the baculovirus glycoprotein GP64.";
Virology 186:640-646(1992).
-: FUNCTION: POSSIBLE ROLE IN ENDOCYTOTIC FUSION EVENTS DURING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | Deam; PF03273; Baculo_gp64. | Deam; PF03273; Baculo_gp64; 1. | Deam; Deam; Deam, D
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-!- SIMILARITY: TO DHORI VIRUS ENVELOPE GLYCOPROTEIN AND TO
BACULOVIRUSES MAJOR ENVELOPE GLYCOPROTEIN (P64/P67).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 512; 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Envelope glycoprotein precursor (Surface glycoprotein 75).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thogoto virus (isolate SiAr 126) (Tho).
Viruses, ssRNA negative-strand viruses; Orthomyxoviridae;
Thogotovirus.
VCBI_TAXID=126796;
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Pred. No.
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62.5%;
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PIR; A40821; VGIVTH.
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               6; Conservative
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                                                                                               3 YENVGMY 9
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nes 5; Conser
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Matches
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July 20, 2004, 15:36:14; Search time 16 Seconds (without alignments) 54:108 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                   283366
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                283366 seqs, 96191526 residues
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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45
1 XLYENVGMY 9
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Perfect score: 6
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	Description	deoxyribodipyrimid	hexon protein - hu	spike glycoprotein .	hexon protein - hu	hemagglutinin - In	cyanamide hydratas	hexon protein - hu	probable diphospha	inin p	hexon protein - hu	hypothetical prote	hypothetical prote	ctin-fi	£22b7.3 protein -	nitrate-inducible	formate dehydrogen	hypothetical prote	protein W10G11.17	ABC transporter at	myosin I myoA - Em	hypothetical prote	aspartate carbamoy	N5-(carboxyethy1)o	hypothetical prote	magnesium and coba	hypothetical prote	avermectin-sensiti	F390	envelope glycoprot
or the state of	ID	S67298	837217	VGVNSG	S33942	PL0161	A39365	839296	F70190	HMIV2	S57637	B81136	H81883	A55883	S44632	F83044	A64042	T33774	G88103	A99574	A56511	18	D64497	₹#	7226	9712	B81380	S50865	A64891	VGIVTH
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asparagine synthas	coat protein gpl -	hypothetical prote	alpha-glucosidase	hypothetical prote	hypothetical prote	hypothetical prote	neural adhesion pr	contactin 1 precur	neuronal cell surf	contactin precurso	hypothetical prote	conserved hypothet	hypothetical prote	hypothetical prote	Ig kappa chain pre	
G95899	S49901	T33708	H90486	T20550	AI1876	T33824	JC4211	A54744	S05944	A57112	D86157	E64400	H89847	H85138	S14237	
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591	661	688	693	700	739	852	1018	1018	1020	1021	1181	221	224	231	234	
71.1	71.1	71.1	71.1	71.1	71.1	71.1	71.1	71.1	71.1	71.1	71.1	68.9	689	68.8	6.89	
32	32	32	32	32	32	32	32	32	32	32	32	31	31	31	31	
30	31	32	33	34	35	36	3.7	38	39	40	41	42	43	. 44	45	

# ALIGNMENTS

RESULT 1 S67298 deoxyribodipyrimidine photo-lyase (EC 4.1.99.3) - yeast (Saccharomyces cerevisiae) NjAlernate names: protein 06771; protein YOR386w
Cipecies: SacurationNyes Circletaine Cipace: 12-Jul-1990#Sequence_revision 12-Jul-1996 #text_change 20-Jun-2000 CiAccession: S67298; A23964; A24046 R;Delius, H.; Hebling, U.; Hofmann, B.
submitted to the Protein Sequence Database, July 1996 A.Reference number: S67261
A; More saston: 30, 20, 20, 20, 20, 20, 20, 20, 20, 20, 2
A,Cross-references: EMBL:Z75294; NID:g1420830; PIDN:CAA99718.1; PID:g1420831; MIPS:YOR386 A;Experimental source: strain S288C P. Venn: B I amount of a b.
Rizabul, A., Dangevers, O.A. General 36, 43-40-1985 A.mitla. Homolock, between the photographication genes of Saccharomyces cerevisiae and Esc
A;Molecasion: Aziona A;Molecasion: Aziona A:Residues: 1-76: /a/,78-164./8/,166-168./T/,170-199./S/,201-350,/R/,352-364,/E/,366-472,/
A; Cross-references: EMEL:M11578; NID:g172169; PIDN:AAA34875.1; PID:g172170
A;Title: Sequence of the Saccharomyces cerevisiae PHR1 gene and homology of the PHR1 phot A;Reference number: A24046; MUID:86067229; PMID:3906569
A,Accession: A24046
A;Molecule Type: DNA A;Residues: 1-565 <san></san>
A;Cross-references: EMBL:X03183; NID:g4175; PIDN:CAA26944.1; PID:g4176
C;Genetics: A;Gene: SGD:PHR1
A;Cross-references: SGD:S0005913; MIPS:YOR386w A:Man position: 15R
C,Superfamily: deoxyribodipyrimidine photo-lyase C,Keywords: carbon-carbon lyase
. 00 03000
4.7; Length 30 4.7; ches 0; Indels
QY 2 LYENVGMY 9
Db 87 LYDNVGLY 94
RESULT 2
53/21/ hexon protein - human adenovirus 31 (fragment) C;Species: Mastadenovirus h31 (human adenovirus 31)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 26-Aug-1999

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cyanamide hydratase (EC 4.2.1.69) - fungus (Myrothecium verrucaria)
C;Species: Myrothecium verrucaria
C;Species: Myrothecium verrucaria
C;Date: 06-Mar-1992 #sequence_revision 06-Mar-1992 #text_change 15-Sep-2000
C;Accession: A39365
R;Maier-Greiner, U.H.; Obermaier-Skrobranek, B.M.M.; Estermaier, L.M.; Kammerloher, W.; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 88, 4260-4264, 1991
A;Title: Isolation and properties of a nitrile hydratase from the soil fungus Myrotheciun A;Reference number: A39365, MUID:91239547; PMID:2034671
A;Accessius preliminary
A;Retus: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A) Experimental source: strain A/JAP/305/57
C; Comment: This protein plays a major role in initiation of infection and in the pathoger C; Superfamily: influence virus hemagglutinin
C; Keywords: hemagglutinin
F;1-20/Region: immunodominant site recognized by T-lymphocytes
                                                                                                                                                                                                                                                                                                                                       RiSweetser, M.T.; Braciale, V.L.; Braciale, T.J.

- Exp. Med. 170, 1357-1368, 1388

Affile: Class I major histocompatibility complex-restricted T lymphocyte recognition of A.Reference number: PL0161; MUID:90010790; PMID:2477491
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hecon protein - human adenovirus 4
Cispecies: Mastadenovirus h4 (human adenovirus 4)
Cispecies: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
Cistate: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
Cistating-Akerblom, P.; Adrian, T.
Ripring-Akerblom, P.; Adrian, T.
A;Reference number: 539296
A;Reference number: 539296
A;Accession: 539296
                                                                                                                                                                                                              hemagalutinin - Influenza H2N2 (fragment)
C;Species: influenza H2N2
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-May-1997
C;Accession: PL0161
  Gaps
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ilarity 75.0%;
Conservative 1
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Matches 6; Conservative
                                                                                                        440 LYSNVGLY 447
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Accession: PL0161
A;Molecule type: mRNA
A;Residues: 1-20 <SWE>
                                              2 LYENVGMY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 spike glycoprotein g precursor - sigma virus
C; Species: sigma virus
A; Note: host Drosophila melanogaster
C; Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 16-Jul-1999
C; Accession: A27150
R; Teninges, D.; Bras. Herreng, F.
A; Gen. Virol. 68, 2625-2638, 198
A; Title: Rhabdovirus sigma, the hereditary CO-2 sensitivity agent of Drosophila: nucleot
A; Reference number: A27150; MUID:88034947; PMID:2822842
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hexon protein - human adenovirus 12
hexon protein - human adenovirus 12
C;Species: Mastadenovirus h12 (human adenovirus 12)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
R;Sprengel, J.
Submitted to the EMBL Data Library, June 1993
A;Reference number: S33928
A;Reference number: S33942
A;Status: preliminary
C;Accession: S37217
Submitted to the EMBL Data Library, September 1993
A;Reference number: S37213
A;Accession: S37217
A;Accession: S37217
A;Accession: S37217
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-references: EMBL:X74661, NID:g402765; PIDN:CAA52725.1; PID:g402766
C;Superfamily: adenovirus hexon protein
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A; Status: DNA
A; Molecule type: DNA
A; Residues: 1-919 cSPR>
A; Residues: 1-919 cSPR>
A; Cross-raferences: EMBL:X73487; NID:g313361; PIDN:CAA51891.1; PID:g313376
C; Superfamily: adenovirus hexon protein
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A, Molecule type: genomic RNA
A, Molecule type: genomic RNA
A, Residues: 1-526 «TEN»
A, Cross-references: GB:X06171; NID:g61818; PIDN:CAA29536.1; PID:g61819
G) Genetics:
A, Gene: G
A, Cross-references: FlyBase:FBgn0015809
C, Superfamily: Tabadovirus spike glycoprotein G
C, Superfamily: Tabadovirus spike glycoprotein G
C, Storefamily: Tabadovirus spike glycoprotein G
C, Storefamily: Tabadovirus spike glycoprotein G
C, Storefamily: Tabadovirus spike glycoprotein G
F, 117/Domain: signal sequence #status predicted «SIG»
F, 499-515/Domain: transmembrane #status gredicted «TMN»
F, 499-515/Domain: transmembrane #status gredicted «TMN»
F, 499-515/Domain: carbohydrate (Asn) (covalent) #status predic
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Pred. No. 12;
2; Mismatches
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22;
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Pred. No.
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Best Local Similarity 75.v
6; Conservative
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LYOSVGMY 358
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Best Local Similarity
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Best Local Similarity
Matches 6; Conserv
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Frettelln, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Accession: B81136
A;Reture: preliminary
A;Residues: 1-29 < TET>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GB:AE002098; NID:g7226204; PIDN:AAF41373.1; PID:g7226208
B, strain MC58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein NMB0968 [imported] - Neisseria meningitidis (strain MC58 serogroup C,Species: Neisseria meningitidis C,Date: 31-Mar-2000 #text_change 19-Jan-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cispecies: Mastadenovirus 4
Cispecies: Mastadenovirus 4
Cispecies: Mastadenovirus h4 (human adenovirus 4)
Cispecies: Mastadenovirus h4 (human adenovirus 4)
Cispecies: Mastadenovirus h4 (human adenovirus 4)
Cispecies: S57637
Ribring-Akerblom, P.; Trijssenaar, J.; Adrian, T.
Submitted to the EMBL Data Library, February 1995
A;Reference number: S57637
A;Recession: S57637
A;Accession: S57637
A;Accession: S7637
A;Status: preliminary
A;Nolecule rype: DNA
A;Residues: 1-936 < PRI
A;Residues: 1-936 < PRI
A;Cross-references: EMBL:X84646; NID:g886486; PIDN:CAAS9139.1; PID:g886487
C;Superfamily: adenovirus hexon protein
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      F;1-15/Domain: signal sequence #status predicted <SIG>
F;16-39/Product: hemagglutinin chain HA1 #status predicted <HA1>
F;341-562/Product: hemagglutinin chain HA2 #status predicted <HA2>
F;551,558,561/Binding site: palmitate (Cys) (covalent) #status predicted
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                                                                                                                                                    Score 35; DB 1; Length 562; Pred. No. 21; 1; Mismatches 1; Indels
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                                                                                                                                                       77.8%;
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A;Experimental source: serogroup
                                                                                                                                                                                                                   Conservative
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Best Local Similarity
Matches 6; Conserv
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Matches 5; Conserv
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C;Genetics:
A;Gene: NMB0968
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: B81136
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Best Local S:
Matches 6,
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S57637
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C;Species: influenza A virus

A;Variestain A/Japan/305/57[H2]

C;Date: 24: strain A/Japan/305/57[H2]

C;Date: 28-Feb-1981 #sequence_revision 28-Feb-1981 #text_change 16-Jul-1999

C;Accession: A04062; S12270

R;Gething, M.J.; Bye, J.; Skehel, J.; Waterfield, M.

R;Gething, M.J.; Bye, J.; Skehel, J.; Waterfield, M.

A;Retence number: A93233; MUD:81030852; PMID:7421990

A;Accession: A04062

A;Accession: A04062

A;Accession: A04062

A;Accession: A04062

A;Accession: A04062

A;Experimental source: strain A/Japan/305/57[H2]

R;Nacve, C.W.; Williams, D.

EMBO J: 985-3866, 1990

A;Title: Fatty acids on the A/Japan/305/57 influenza virus hemagglutinin have a role in A;Reference number: S12270; MUID:91065313; PMID:2249653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable diphosphate-fructose-6-phosphate 1-phosphotransferase (BC 2.7.1.90) - Lyme diserbrobable diphosphate-fructose-6-phosphate 1-phosphotransferase (BC 2.7.1.90) - Lyme diserbrobable diphosphate-fructose-6-phosphate 1-phosphotransferase (BC 2.7.1.90) - Lyme diserbrobable disease spirochete)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Aug-2003
C;Accession: F70190
C;Accession: F70190
#sequence_revision 10-Sep-1999 #text_change 04-Aug-2003
C;Accession: F70190
D; Peterson, J; Kerlavage, A.R.; Quadechubush, J; Salzberg, S.; Hathigra, R.; White Son, D.; Peterson, J; Kerlavage, A.R.; Quadechubush, J; Salzberg, S.; Hatch, B.
Agura 390, S80-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Authors: Smith, H.O.; Venter, J.C.
A;Attle: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Accession: F70190
A;Status: P70190
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Resiques: 1-448 cKLE>
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C, Superfamily: pyrophosphate-dependent phosphofructokinase, Eh/PPi-PFK type, 6-phosphofr
C, Keywords: phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Cross-references: GB:AE001172, GB:AE000783; NID:g2688654; PIDN:AAC67070.1; PID:g268865
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A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-47 < PRI>
A,Cross-references: BMBL:X76550, NID:g434903; PIDN:CAA54052.1; PID:g434904
C,Superfamily: adenovirus hexon protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77.8%; Score 35; DB 1; Length 448; 62.5%; Pred. No. 16; 1.1ve 3; Mismatches 0; Indels
                                                                                                                                                                                    Length 447;
                                                                                                                                                                                                                                                1; Indels
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A;Residues: 510-562 kNAE>
A;Experimental source: strain A/Japan/305/57 (H2N2)
C;Superfamily: influenza virus hemagglutinin
                                                                                                                                                                                Score 35; DB 2
Pred. No. 16;
1, Mismatches
                                                                                                                                                                                77.8%;
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Best Local Similarity 62.5-
has 5; Conservative
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Matches 6; Conservative
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Search completed: July 20, 2004, 15:45:07 Job time: 16 secs
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                                                                21 YENLGMF 27
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                    3 YENVGMY 9
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                    à
C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C;Accession: H81883
R;Parchill, J. Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morei, Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000
A;Reference number: A8175; MUD:2022556; PMID:10761919
A;Accession: H81883

                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB84427.1; PID:g737995
A,Experimental source: serogroup A, strain Z2491
C,Genetics:
A,Gene: NMA1165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     action—filament-associated protein 120k form - chicken (fragment)
C,Species: Gallus gallus (chicken)
C,Species: Gallus gallus (chicken)
C,Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
C,Date: 19-Oct-1995 #sequence_revision 19-Oct-1995
C,Date: 10-Oct-1995 #sequence_revision 19-Oct-1995
C,Date: 10-Oct-1995 #sequence_revision 19-Oct-1995
C,Date: 19-Oct-1995
R,Flynn, D.C.; Koay, T.C.; Humphries, C.G.; Guappone, A.C.
J. Biol. Chem. 270, 3894-3889, 1995
A,Title: ARPA-120. A variant form of the Src SHZ/SH3-binding partner AFAP-110 is detected.
A,Reference number: A55883; MUD:95181352; PMID:7876134
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C;Species: Caenorhabditis elegans
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Sep-1997
C;Accession: S44632
R;Anderson, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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A, Molecule type: DNA
A, Residues: 1-99 cAND>
A, Cross-references: EMBL:L12018; NID:g156298; PID:g156303
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A;Description: Sequence of the C. elegans cosmid F22B7.
A;Reference number: S44628
A;Accession: S44632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 34; DB 2;
Pred. No. 1.5;
3; Mismatches
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62.5%;
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Best Local Similarity 62.5
Matches 5; Conservative
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A;Molecule type: mRNA
A;Residues: 1-150 <FLV3
A;Cross-references: GB:L20302
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LYKNLGLY 34
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Best Local Similarity
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A; Introns: 25/1; 81/3
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C;Species: Pseudomonas aeruginosa C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 02-Aug-2002 C;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 02-Aug-2002 C;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 02-Aug-2002 R;Stover C.K.: Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bridaman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.Y. Mature 406, 959-964, 2000 A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathog A,Accession: F33044
A,Status: preliminary
A,Status: preliminary
A,Residues: 1-309 <STOA,Cross-references: GB-AE004894; GB:AE004091; NID:g9951076; PIDN:AAG08197.1; GSPDB:GN001:
A,Experimental source: strain PA01
C;Superfamily: formate dehydrogenase, nitrate-inducible, beta chain; ferredoxin 2[4Fe-4S]

Gaps ., Length 309; 1; Indels Ouery Match 73.3%; Score 33; DB 2; Best Local Similarity 71.4%; Pred. No. 29; Matches 5; Conservative 1; Mismatches

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2 LYENVGMY 9
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                                                                                                                                                                                                        July 20, 2004, 15:42:39; Search time 18 Seconds (without alignments) 25.813 Million cell updates/sec
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Seguence 2
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
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6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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PCT-US95-08565-8
US-08-146-145-6
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US-08-471-939-31
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US-08-471-939-31
US-08-471-939-31
US-08-471-939-31
US-08-471-066-31
US-08-471-066-31
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                               - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1 XLYENVGMY 9
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Maximum DB
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13869, A
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US-08-471-800-22
US-08-471-800-22
US-09-134-000C-3547
US-09-489-039A-13869
US-08-449-112-4
PCT-US-95-6556-4
US-08-770-802-8
US-09-991-36-8
US-09-970-802-8
US-09-970-802-8
US-09-970-802-8
US-09-619-35-10
US-08-408-420A-6
US-08-408-420A-6
US-08-408-420A-6
US-08-45-052-2
US-08-6527-227A-7
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## ALIGNMENTS

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THE TALL IN CORMAND TO GRAMMONE, ADPLICANT: CASHMONE, ADPLICANT: Ahmad, Margaret
APPLICANT: Ahmad, Margaret
APPLICANT: Ahmad, Margaret
APPLICANT: Lin, Chentao
TITLE OF INVENTION: Blue Light Photoreceptors and Methods of
TITLE OF INVENTION: Using the Same
NUMBER OF SEQUENCES: 22
CORRESPONDENCES:
CORRESPONDENCE ADDRESS:
STREET: WoodGoock, Washburn, Kurtz, Mackiewicz & No. 5824859ris
STREET: One Liberty Place, 46th floor
STREET: One Liberty Place, 46th floor
STREET: One Liberty Place, 46th floor
STREET: ONE STREET: USA
STREET: USA
ZIP: 19103
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

COMPUTER: IBM PC Compatible

COMPUTER: IBM PC COMPACIBLE

COMPATION SYSTEM: PATENTIN Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/272,255

FILING DATE: 08-UL-1994

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Leary Ph.D., Kathryn

REFERENCE/DOCKET NUMBER: 36,317

REFERENCE/DOCKET NUMBER: 19N-1795

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-3100

TELEPRA: (215) 568-3100

TELEPRA: (215) 568-3100

TELEPRA: (215) 568-3109

TELEPRA: (215) 568-3109
; Sequence 8, Application US/08272255; Patent No. 5824859; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: protein
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Best Local Similarity
Matches 6; Conserv
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88 LYDNVGLY

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Sequence 6, Application US/08146145
; Sequence 6, Application US/08146145
; Patent No. 5747269
; GENERAL INFORMATION:
APPLICANT: Ranmensee, Hans-Georg
APPLICANT: Ralk, Kirsten
APPLICANT: Stevanovic, Stefan
APPLICANT: Stevanovic, Stefan
TITLE OF INVENTION: MOLECULES
; TITLE OF INVENTION: MOLECULES
; TUTLE OF INVENTION: MOLECULES
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146,145
FILING DATE: 17-NOV-1993
ATTORNEY/ACCTION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Nikaido, Marmelstein, Murray & Oram STREET: 655 Fifteenth Street N.W. Suite 330 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: predicted hexon protein sequence;
NAME/KEY: for human Adenovirus 12
US-08-788-674-4
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: 1BM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/788,674
FILING DATE: 24-JAN-1997
                                                                                                                                                                                                FILING DATE: 24-JAN-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Olstein, Elliot M.
REGISTRATION NUMBER: 24,025
REFRENCE/DOCKET NUMBER: 27101
TELEFAN: 973-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 919 amino acids
TYPE: amino acid
STRANDEDNES:
TOPOLOGY: linear
MOLECULE TYPE: protein
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NAME: Kitts, Monica C.
REGISTRATION NUMBER: 36,1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 75.0
Matches 6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   440 LYSNVGLY 447
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COUNTRY: U.S.A.
ZIP: 20005-5701
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US-08-146-145-6
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                                                                                        GENERAL INFORMATION:
APPLICANT: Cashmore, Anthony R.
APPLICANT: Ahmad, Margaret
APPLICANT: Lin, Chentao
TITLE OF INVENTION: Blue Light Photoreceptors and Methods of
TITLE OF INVENTION: Using the Same
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSE: Moodcock, Mashburn, Kurtz, Mackiewicz & Norris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84.4%; Score 38; DB 5; Length 566; 75.0%; Pred. No. 7.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Recent Release #1.0, Version #1.25
CURRENT APPLICATION DATA
APPLICATION NUMBER: PCT/US95/08565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Roy, Soumitra
IITLE OF INVENTION: Adenoviruses Having Altered
IITLE OF INVENTION: Hexon Proteins
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSE: Carella, Byrne, Bain,
ADDRESSE: Gilfillan, Cecchi, Stewart &
ADDRESSE: Olstein
STREET: 6 Becker Farm Road
CITY: Roseland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,255
FILING DATE: 08-UUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Leary Ph.D., Kathryn
REGISTRATION NUMBER: 36,317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: UPN-1795
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-788-674-4; Sequence 4, Application US/08788674; Patent No. 5922315; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
.INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 566 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 75.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88 LYDNVGLY 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 LYENVGMY 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino a STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
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STATE: Ne
COUNTRY:
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Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 LYQNVGTY 10
                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                2 LYENVGMY 9
                                                                                                                                                                                                                                                                                                                                                          US-08-480-190-38
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US-08-488-379-38
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                                                                                                                                                             Score 35; DB 1; Length 9; Pred. No. 3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 38, Application US/08480190;
Patent No. 5827516
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Dario A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Dario A. A. Vignali
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMONODULATORY PEPTIDES
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U.S.A.
ZIP: 02110-2804
CMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
TELECOMMUNICATION INFORMATION:
                                                                                                                                                          Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative
                       TELEFAX: (2026/88-4810
; INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 9 amino acids TYPE: amino acid TOPOLOGY: linear / MOLECTLE TYPE: peptide US-08-146-145-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 IYENLGVY 13
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               TELEPHONE:
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US-08-480-190-38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 38, Application US/08488379
Patent No. 5880103
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Roman M. Chicz
APPLICANT: Dario A. A. Vignali
APPLICANT: Dario A. A. Vignali
APPLICANT: Lawrence J. Stern
APPLICANT: Lawrence J. Stern
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
IITLE OF INVENTION: INMUNOMODULATORY PEPTIDES
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READALE FORM:
NEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WORTPETECT (Version 5.1)
CURRENT APPLICATION NUMBER: US/08/488,379
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,190
FLING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,255
FLING DATE: June 15,1933
APPLICATION NUMBER: 07/925,460
FILING DATE: AUGUST 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: CLIRK, Paul T.
REGISTRATION NUMBER: 30,162
REFREENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION NUMBER: OS/OS/200,575

CLASSIFICATION DATA:
PRICH APPLICATION DATA:
APPLICATION UNMBER: 08/077,255
FILING DATE: June 15, 1993
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: CLARK, PAUL T.
REGIGSTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
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Gaps
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Sequence 6, Application US/09003287

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Dayne, Usen
APPLICANT: Barbour, Eric
APPLICANT: Meyer, Terry
TITLE OF INVENTION: METHODS FOR IMPROVING TRANSFORMATION EFFICIENCY
FILE REPRENCE: moPAT_moCaH
CURRENT APPLICATION NUMBER: US/09/003,287

CURRENT FILING DATE: 1998-01-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
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                                                                                                                                                                                                                                                                                                                                Sequence 339.795
Sequence 139.795
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Robert G. Urban
APPLICANT: Boman M. Chicz
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 273
CORRESONDERCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 35; DB 5;
Pred. No. 0.74;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Boston
STATE: Massachusetts
COUMTRY: U.S.A.
ZIP: 0.110-2804
COMPUTER READABLE FORM:
COMPUTER: BM PS/2 Model 502 or 558X
COMPUTER: NordPerfect (Version 5.0)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
#PPLICATION NUMBER: PCT/US93/07545
PTI.ING DATE: 19930811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 30,162
REPERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-8906
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/925,460
FILING BATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: CLARK, Paul T.
REGISTRATION NUMBER: 30,162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 LYONVGTY 10
                                                                                                                                                                                 3 LYQNVGTY 10
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                                                                                                                                               2 LYENVGMY 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS
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PCT-US93-07545-38
                                                                                                                                                                                                                                                                                                                          PCT-US93-07545-38
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US-09-003-287-6
                                                                                                                                                                                                                                                                                              RESULT 9
us-09-998-350-1.rai
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Best Local Similarity 75.0%; Pred. No. 0.74;
Matches 6; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INPORMATION:
APPLICANT: Urban, Robert G.
APPLICANT: Urban, Robert G.
APPLICANT: Chica, Roman M.
APPLICANT: Vignali, Dario A.A.
APPLICANT: Stern, Lawrence J.
APPLICANT: Stern, Lawrence J.
APPLICANT: Strominger, Jack L.
TITLE OF INVENTION: ImmUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 276
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSEE: Rish & Richardson, P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: WAS COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE DISKETTE
MEDIUM TYPE: DISKETTE
COMPUTER: DISKETTE
APPLICATION NUMBER: US/08/475,399A
FILING DATE: DISKET ON/925,460
FILING DATE: DATE: DISKET ON/925,460
FILING DATE: DAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 35; DB 2;
Pred. No. 0.74;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 8
US-08-475.399A-36
Sequence 38, Application US/08475399A
; Patent No. 6509033
      Tue Jul 20 16:13:37 2004
                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                       TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LU NO:
LACTÉRISTICS:
LAH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-475-399A-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77.8%;
75.0%;
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TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 75.0
Matches 6; Conservative
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LYQNVGTY 10
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                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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US-08-488-379-38
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Score 35; DB 3; Length 244; pred. No. 12; 1; Mismatches 1; Indels
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Similarity 75.0%; Pred. No. 31;
6; Conservative 1; Mismatches 1; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/080,897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: SCIENCE & TECHNOLOGY LAW GROUP STREET: 75 DENISE DRIVE CITY: HILLSBOROUGH STATE: CALIFORNIA COUNTRY: USA ZIME 940°.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REPERENCE/DOCKET NUMBER: UW97-001
TELECOMUNICATION INFORMATION:
TELEFAX: (650) 343-434
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 362 amino acids
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Persons, Nancy J.
REGISTRATION NUMBER: 40,364
REFERENCE/OCKET NUMBER: 017.95
TELECOMMUNICATION INFORMATION:
TELEPRAN: (510) 559-5731
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/09080897 Patent No. 5985574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: King, Mary-Claire
APPLICANT: Lynch, Eric D.
APPLICANT: Lynch, Eric D.
APPLICANT: Morrow, Jan B.
APPLICANT: Morrow, Jan E.
APPLICANT: Morrow, Jan E.
APPLICANT: Leon, Pedro E.
APPLICANT: Leon, Pedro E.
TITLE OF INVENTION: Modulators
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLG
                                                                                                                                                                                                                                                                                                                      77.8%;
75.0%;
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                 : 244 amino acids
amino acid
GY: linear
                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 75.v
est Local Similarity 75.v
                                                                                                                                                                                                                                                      , MOLECULE TYPE: protein US-09-518-988-2
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0S-09-080-897-6
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APPLICANT: Barbour, Eric
APPLICANT: Barbour, Eric
APPLICANT: Meyer, Terry
TITLE OF INVENTION: METHODS FOR IMPROVING TRANSFORMATION EFFICIENCY
FILE REPERSENCE: mocAT moCAT
CURRENT APPLICATION NUMBER: US/09/003,287
CURRENT FILING DATE: 1998-01-06
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTIN VET: 2.0
SEQ ID NO 8
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Pred. No. 12;
                                                                                                                                                                 77.8%; Score 35; DB 3; Length 244; 75.0%; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2 Application US/09518988
; Sequence 2 Application US/09518988
; Patent No. 6268547
; GENERAL INFORMATION:
APPLICANT: Weeks, James T.
TITLE OF INVENTION: CYANAMIDE HYDRATASE GENE
TITLE OF INVENTION: CYANAMIDE HYDRATASE GENE
NUMBER OS SEQUENCES: 2
NUMBER OS SEQUENCES: 2
ADDRESSEE: Nancy J. Parsons
STREET: 800 Buchanan St.
CITY: Albany
STATE: CA
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/518,988 FILING DATE:
                                                                                                                                                                                                         1; Mismatches
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COMPUTER READABLE FORM:
MEDIUM TYPE: FORM:
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/873,001
                                                                                                                                                                                                                                                                                                                                                 RESULT 11
US-09-003-287-8
; Sequence 8, Application US/09003287
; Patent No. 6096947
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LENGTH: 244
; TYPE: BRT
; ORGANISM: Myrothecium verrucaria
US-09-003-287-8
                                                                                         ) TYPE: PRT
; ORGANISM: Myrothecium verrucaria
US-09-003-287-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative
  NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
                                                                                                                                                                                                           6; Conservative
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Best Local Similarity
Matches 6; Conserv
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US-09-518-988-2
                                                                   LENGTH: 244
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Score 33; DB 4; Length 310;
Pred. No. 42;
1; Mismatches 1; Indels
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1999-07-27
SEQ ID NO 27339
LENGTH: 310
                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: July 20, 2004, 15:45:37 Job time : 19 secs
                                                                                                                                                                     TYPE: PRT CRGANISM: Pseudomonas aeruginosa US-09-252-991A-27339
                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                 205 YENAGLY 211
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Patent No. 6551795

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
MUCLEIC ACID AND AMINO ACID
FILE OF INVENTION:
FILE PERERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A
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                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 75 DENISE DRIVE CITY: HILLSBOROUGH STRATE: CALIFORNIA COUNTRY: USA
                                                                                                                                                            ; Sequence 6, Application US/09323735
; Patent No. 6197932
; GENERAL INFORMATION;
; APPLICANT: King, Mary-Claire
APPLICANT: Lynch, Eric D.
APPLICANT: Lee, Ming
APPLICANT: Melcsh, Piri L.
APPLICANT: Welcsh, Piri L.
APPLICANT: Leon, Pedro E.
; APPLICANT: Leon, Pedro E.
; APPLICANT: Leon, Pedro E.
; TILL OF INVANTION: Modulators of Actin NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/323,735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UW97-001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/080,897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UNY
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (650) 343-4341
TELEPAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 362 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 362 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                              ||||:| |
248 LYENLGEY 255
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248 LYENLGEY 255
                        2 LYENVGMY 9
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US-09-252-991A-27339
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US-09-323-735-6
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MEDLINE=96074506; PubMed=7491755;
Landes-Devauchelle C., Bras F., Dezelee S., Teninges D.;
"Gene Z of the sigma rhabdovirus genome encodes the P protein, gene 3 encodes a protein related to the reverse transcriptase o retroelements.";
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EMBL; X91062; CAA62517.1; -.
InterPro; IRR01903; Rhabd_glycop.
Ffan; PF0974; Rhabdo glycop; 1.
SEQUENCE 540 AA; 60771 MW; 7A0B553D1EASE98A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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                  09997B2
09997B3
09997B3
099907B1
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09WQW7
09WQW5
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Q9WQW0
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01,
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01-NOV-1996 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
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SEQUENCE FROM N.A.
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Matches 6; Conserv
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    Glycoprotein.
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Q813V8
ID Q813V8
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Q88452
    ACCOORDING TO THE SECOND SECON
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Q91f30 bovine aden
Q91ff4 influenza a
Q91ff2 influenza a
Q91ff6 influenza a
Q91ff6 influenza a
Q91ff7 influenza a
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Q91ff8 influenza a
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                                                                                                                                                      (without alignments)
78.880 Million cell updates/sec
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                                                                                                                                July 20, 2004, 15:34:04; Search time 36 Seconds
                  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pplant:*
sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_rvirus:*
sp_bacteriap:*
                                                                                                                                                                                                                                                                                                             Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mammal:*
                                                                                               using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sp_organelle:*
sp_phage:*
                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 200000000
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45
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                                                                                                                                                                                                                                                    1 XLYENVGMY 9
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Match Length
                                                                                             protein search,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing:
                                                                                                                                                                                                            Title:
Perfect score:
                                                                                                                                                                                                                                                                                       Scoring table:
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                                                                                               protein
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                                                                                                                                  Run on:
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Gaps

; 0

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80.0%; Score 36; DB 12; Length 914; 75.0%; Pred. No. 1.6e+02; ive 1; Mismatches 1; Indels
Pfam; PF01065; Adeno hexon; 1.
Pfam; PF03678; Adeno hexon C; 1.
ProDom; P002815; Adeno hexon; 1.
NON TEX 914 914
SEQUENCE 914 AA; 103905 MW; SSOBE006997739CD CRC64;
                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 71.4
Matches 5, Conservative
                                                                                                                                                              6; Conservative
                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Multidrug pump KlPDR5.
                                                                                                                                                                                                                                         434 LYSNVGLY 441
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                                                                                                                                                                                                   2 LYENVGMY 9
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                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=28985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                           Q96WM8
                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                 RESULT 4
Q96WM8
ID Q96WM
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                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N. P. Berriman M., Churcher C., Harris B., Harris D., MEDLINE=22255708; PubMed=12368867;
A Hall N., Pain A., Berriman M., Churcher C., Harris B., Harris D., Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K., Buckee C.O., Burrows C., Cherwach I., Chillingworth C., Croin A., Davis B., Goodlew Z., Clark L., Clark R., Corton C., Croin M., Davis R., Goodlew I., Goole A., Goodlew I., Gwilliam R., Hamlin N., Hance Z., Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P., Hance Z., Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A., Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N., Line A., Maddison M., Mclean J., Mooney P., Moulle S., Murphy L., Oliver K., Ormond D., Price C., Quall M.A., Rabbinowitsch E., Asjandrem M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M., Seeger K., Shars S., Stevens K., Asjandres M., Shalson J., Whitehead S., Woodward J., Sulston J.E., Craig A., Newbold C., Barrell B.G., Squares S., Stevens K., Squares S., Stevens K., Squares L., Craig A., Newbold C., Barrell B.G., Squares S., Stevens K., Squares A., Squares R., Squ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hexon protein (Fragment).

Bovine ademovirus type 10 (Mastadenovirus bos10).

Viruses; dsDNA viruses, no RNA stage; Ademovirjadae; Mastadenovirus.
                                                                                                                                                                                                                          Devin K., Baker S., Davies P., Mungal K., Berriman M., Pain A., Hall N., Bowman S., Churcher C., Quail M., Barrell B.; Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
                                                                                                                    Plasmodium falciparum (isolate 3D7).
Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBI_TaxID=36329,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 848;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match

Best Local Similarity 71.4%; Pred. No. 1.5e+02;
Matches 5; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=78-5371;
Lebmkuhl H.D., Hobbs L.A.;
Lebmkuhl H.D., Hobbs L.A.;
EMBL, AF28274; AAF8236.1; --
HSSP, P03277; LDHX.
GO, GO:0019028; C:viral capsid; IEA.
GO; GO:0000028; F:structural molecule activity; IEA.
InterPro; IPR000736; Adeno_hexon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, AL929352, CAD51514.1, -
GO: GO:0003676; F:nucleic acid binding; IEA.
InterPro: IPROON56; F:nucleic acid binding; IEA.
Fine ProON76; F:nucleic acid binding; IEA.
SMART; SM0360; F:NM, 1.
PROSTITE; PS50102; F:NM, 1.
SEQUENCE 848 AA; 98382 WW; A7989468AB9FEF89 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-00T-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                           01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypochetical protein, conserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                914 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 419:527-531(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  486 YDNIGMY 492
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SEQUENCE FROM N.A.
                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                            PFE0750C
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J. Bacteriol. 183:393-3948(2001).
-: SIMILMAITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
-: SIMILMAITY: BELONGS TO THE ABC TRANSPORTER FAMILY.

GO; GO:0005524; FAITP binding: IEA.
GO; GO:0004009; F.AITP binding cassette (ABC) transporter acti. . .; IEA.
GO; GO:0000166; F.AITP-binding cassette (ABC) transporter acti. . .; IEA.
GO; GO:0006180; P.AITP-binding cassette (ABC)
INCORGANO; P. transport; IEA.
InterPro; IPR003593; AAA, ATPASe.
InterPro; IPR003439; ABC_transporter.
InterPro; IPR003585; PAP.
InterPro; IPR003585; PAP.
InterPro; IPR003585; PAP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kluyveromyces lactis (Yeast).
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes;
Saccharomycetales, Saccharomycetaceae, Kluyveromyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
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Pred. No. 2.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QGIFF9 PRELIMINARY; PRT; 339 AA.

Q19FF9;

Q10CT-2000 (TEMBLrel. 15, Last sequence update)

Q1-0CT-2003 (TEMBLrel. 25, Last annotation update)

Q1-0CT-2003 (TEMBLrel. 25, Last annotation update)

Influenza A virus (A/Davis/1/57(HZN2)).

Viruses; SSRNA negative-strand viruses; Orthomyxoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1525 AA; 172140 MW; C6DFA243718186D2 CRC64;
                                                                                                                                                                                          Last sequence update)
Last annotation update)
PRT; 1525 AA
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                                                                                                                                 Created)
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MEDLINE=21289079; PubMed=11395457;
Chen X.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80.0%;
71.4%;
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mammals...;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.

Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION (BY SIMILARITY).

-!- SUBUNIT: HOWOTRINEN: BACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HA2) LINKED BY A DISULFIDE BOND (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.

REMBL; AF270726; AAF82110.1; --

GO, GO:0019031; C:viral envelope; IEA.

RR InterPro; IPR003969; Capsid, hemag.

InterPro; IPR003969; Capsid, hemag.

RR InterPro; IPR003969; Hemagglutin.; 1.

PFRIM: PRODOM; PR000225; Hemagglutin.; 1.

RR PRINTS; PR00329; Hemagglutin.; 1.

RR PRODOM; PR000225; Hemagglutin.; 1.

RR PRODOM; PR000225; Hemagglutin.; 1.

RR NOW IRR 339 AA; 37964 MW; 97239D60CDIFFD08 CRC64;
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STRAIN=A/RI/5+/57;
Matroseovich M., Tuzikov A., Bovin N., Gambaryan A., Klimov A.,
Castrucci M.R., Donatelli I., Kawaoka Y.,
"Early alterations of the receptor-binding properties of Hl, H2 and H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MATCOSOVICH M., Tuzikov A., Bovin N., Gambaryan A., Klimov A.,
Matrosovich M.R., Donatelli I., Kawaoka Y.,
Castrucci M.R., Donatelli I., Kawaoka Y.,
"Early alterations of the receptor-binding properties of H1, H2 and
avian influenza virus hemagglutinins after their introduction into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77.8%; Score 35; DB 12; Length 339; 75.0%; Pred. No. 90; 1; Mismatches 1; Indels
      Length 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Headglutinin (Fragment).

Influenza A virus (AVvictoria/15681/59 (H2N2)).

Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;

Influenza A viruses; Influenzavirus A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   991FF6 PRELIMINARY; PRT; 339 AA.
010FF6;
01-0CT-2000 (TERMELTEL: 15, Created)
01-0CT-2000 (TERMELTEL: 15, Last sequence update)
01-0CT-2003 (TERMELTEL: 25, Last annotation update)
Hemagglutinin (Fragment).
Influenza A virus (A/RI/5+/57 (H2N2)).
Yutuses, SERNA negative-strand viruses; Orthomyxoviridae; Influenza A viruses; Influenza Aviruses; Influenzavirus A.
                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Query Match

77.8%; Score 35; DB 12;
Best Local Similarity 75.0%; Pred. No. 90;
Matches 6; Conservative 1; Mismatches 1.
                                                                                                                                                                                                                                                                                                                                                 339 AA
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Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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204 LYQNVGTY 211
                                                                                                                             2 LYENVGMY 9
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                                                                                                                                                                                                                                                                                      RESULT 7
Q9IFF2
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Q9IFF6
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Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INPECTION (BY SIMILARITY).

CELL: SUBUNIT: HOMOTRIMER EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HA2) LINKED BY DISULFIDE BOND (BY SIMILARITY).

CHILARRITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.

REBL: AR270724, AAR82108.1, -..

RO; GO: 0019031; G:viral envelope; IEA.

InterPro; IPRO01834; Hemagglutn.

R Ffam; PF00509; Hemagglutnin; 1.

PRINTS; PR00329; HEMAGGLUTINI, 1.

PRINTS; PR00329; Hemagglutnin; 1.

PRODOM; PD000225; Hemagglutnin; 1.

R ENVELORE TOTOLE; Hemagglutnin; 1.

M ENVELORE TOTOLE; Hemagglutnin; 1.

TON TER. 339 AA; 37893 MW; D59A26IEIEB9B621 CRC64;
                                                                                                                                                                                                                                                                                                          mandale...

Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION (BY SIMILARITY).

-!- SUBUNIT: HOWOTRIMER: EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAL AND HAZ) LINKED BY D SIGULFIDE BOND (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.

R MGD; GO:0019031; C:viral envelope; IEA.

InterPro; IPRO09980; Capsid hemag.

InterPro; IPRO09980; Capsid hemag.

InterPro; IPRO0990; Hemagglutin...

PRODOM; PRO00225; Hemagglutin...

PRINTS; PRO0329; Hemagglutin...

PRODOM; PRO00225; Hemagglutin...

R Envelope protein; Glycoprotein; Hemagglutinin.

TOW TER 339 AA; 37810 MW; 7D35925ED7538B08 CRC64;
                                                                                                                                                                                                                             H3
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STRAIN=A/Malaya/16/58;
Matrosovich M., Tuzikov A., Bovin N., Gambaryan A., Klimov A.,
Castrucci M.R., Donatelli I., Kawaoka Y.;
"Early alterations of the receptor-binding properties of H1, H2 and
avian influenza virus hemagglutinins after their introduction into
                                                                                                                          STRAIN=A.Navis1/57;
STRAIN=A.Navis1/57;
Matroscovich M., Tuzikov A., Bovin N., Gambaryan A., Klimov A.,
Matroscovich M.R., Donatelli I., Kawaoka W.,
"Barly, alterations of the receptor-binding properties of H1, H2 and
avian influenza virus hemagglutinins after their introduction into
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Pest Local Similarity 75.0%; Pred. No. 90;
Matches 6; Conservative 1; Mismatches 1; Indels
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update).
01-0CT-2003 (TrEMBLrel. 15, Last annotation update).
Hemagdlutinin (Fragment).
Hemagdlutinin (Fragment).
Viruses; SRNA negative-strand viruses; Orthomyxoviridae;
Influenza A viruses, Influenzavirus A.
             Influenza A viruses; Influenzavirus A.
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                                              NCBI_TaxID=220951;
                                                                                                      SECTIENCE FROM N.A.
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339 AA.

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Hemagglutinin (Fragment).
Influenza A virus (Strain A/Ann Arbor/6/60).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza A viruses; Influenzavirus A.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Q9IFF7;
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                     RESULT 10
Q9IFF7
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Q9IFF8
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                          mammals.",

submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO

-!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO

-!- FUNCTION: HEMAGGLUTININ EACH OF THE MONOMERS IS FORMED BY TWO CHAINS

-!- SUBMIT: HOWOTRINER. BACH OF THE MONOMERS IS FORMED BY TWO CHAINS

-!- SIMILARITY: BELONGS TO THE INFLUENCA HEMAGGLUTININ EAMILY.

EMBL: AF270722; AAF82106.1;

-GO; GO:0019031; C:viral envelope; IBA.

InterPro; IPR008980; Capsid hemag.

InterPro; IPR008981; Hemagglutn.
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Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.

Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.

-! FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO

-! CELL RECEPPORS AND EOR INTITATING INECTION (BY SIMILARITY).

-! SUBUNIT: HOMOTRIENER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HA2) LINKED BY A DISULFIDE BOND (BY SIMILARITY).

-! SIMILARITY: BELCANGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.

EMBL; AF270728; AAF82112.1; --

GQ; GQ:0019031; C:viral envelope; IEA.

InterPro; IPRO08980; Capsid hemag.

InterPro; IPRO08980; Capsid hemag.
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avian influenza virus hemagglutinins after their introduction into
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(TremBirel. 15, Last sequence update)
(TremBirel. 25, Last annotation update)
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75.0%; Pred. No. 90;
iive 1; Mismatches
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PRINTS; PR00329; HEMAGGLUTN12.
ProDom; PD000225; Hemagglutn; 1.
Envelope protein; Glycoprotein; Hemagglutinin.
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Pred. No. 90;
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Influenza A virus (A/Chile/6/57 (H2N2)).
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75.0%;
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Query Match
Best Local Similarity 75.v..
6; Conservative
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STRAIN=A/Chile/6/57;
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STRAIN=A/Ann Arbor/6/60;
Matrosovich M., Tuzikov A., Bovin N., Gambaryan A., Klimov A.,
Castrucci M.R., Donatelli I., Rawaoka Y.;
"Early alterations of the receptor-binding properties of H1, H2 and H3
avian influenza virus hemagglutinins after their introduction into
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STRAIN=A/Albany/7/57;
Matrosovich M., Tuzikov A., Bovin N., Gambaryan A., Klimov A.,
Castrucci M.R., Donatelli I., Kawaoka Y.;
"Early alterations of the receptor-binding properties of H1, H2 and H3 avian influenza virus hemagglutinins after their introduction into
                                                                                                                                                                                                                                                                                              Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: HERAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION (BY SIMILARITY).

-!- SUBUNT: HOWOTRIMER. BACH OF THE WONOMERS IS FORMED BY TWO CHAINS (HAI AND HA2) LINKED BY A DISULFIDE BOND (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.

EMBL; AF270721; AAF82105.1; -..

GO; GO:0019031; C:viral envelope; IEA.

InterPro; IPRO08980; Capsid hemag.

InterPro; IPRO01364; Hemagglutn.
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-!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION (BY SIMILABILY).

-!- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HA1 AND HA2) LINKED BY A DISQLIFIDE BOND (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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Influenza A virus (A/Albany/7/57 (H2N2)).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenza A viruses, Influenzavirus A.
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1-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Pred. No. 90;
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PRINTS; PR00329; HEMAGGLUTN12.
ProDom; PD000225; Hemagglutn; 1.
Envelope protein; Giycoprotein; Hemagglutinin.
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75.0%;
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Best Local Similarity 75.01
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Influenza A
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-! FUNCTION: HERAGGLUTININ IS RESPONDIBLE FOR ATTACHING THE VIRUS TO
-!- FUNCTION: HERAGGLUTININ IS RESPONDIBLE FOR ATTACHING THE VIRUS TO
-!- SUBENIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS
(HAT AND HAZ) LINKED BY A DISULFIDE BOND (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
EMBL; AP270723; AAF82107.1; -.
EMBL; AP270723; Caylaid, hemagglutin.
InterPro; IPRO08980; Capsid, hemagglutin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             77.8%; Score 35; DB 12; Length 339; 75.0%; Pred. No. 90;
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01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hemagglutinin (Fragment).
Influenza A virus (A/Albany/6/58(H2N2)).
Viruses; SSRNA negative strand viruses; Orthomyxoviridae;
Influenza A viruses; Influenzavirus A.
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PRINTS; PR00329; HEMAGGLUTN12.
PRODOM; PD000225; Hemagglutn; 1.
Envelope protein; Glycoprotein; Hemagglutinin.
NON TER 339 339
                              GO; GO:0019031; C:viral envelope; IEA.
InterPro; IPR008980; Capsid hemag.
InterPro; IPR001364; Hemagglutn.
PRINTS; PR00329; HEMAGGLUTN12.
ProDom; PD000225; Hemagglutni, 1.
Envelope protein; Glycoprotein; Hemagglutini.
SEQÜENCE 339 As; 37825 WW; OD3E767F9241AA30
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(TrEMBLrel. 15, I
(TrEMBLrel. 25, I
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    EMBL; AF270720; AAF82104.1;
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Matches 6; Conservative
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STRAIN=A/Albany/6/58;
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Q91FG0
ID Q91FG
AC Q91FG
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DT 01-OC
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COSTEPS
TO 091FFS
DT 01-0C
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Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.

Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION (EWS SIMILARITY).

-!- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HALLAND HAZ) LINKED BY A DISULFIDE BOND (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.

EMBL, AF270718; AAF82102.1; --

R GO; GO:0019031; C:viral envelope; IEA.

InterPro; IPR008980; Capsid_hemag.

InterPro; IPR008980; Capsid_hemag.

InterPro; IPR008980; Capsid_hemag.

INTERPRO; PR000129; HEMAGGLUTINI. 1.

PRODOM: PD000225; Hemagglutinin. 1.

R RINTS; PR00129; HEMAGGLUTNI2.

R Brolope protein; Glycoprotein; Hemagglutinin.

T NON TER 339 AA; 37798 MW; PE7698C4DCIDI5E6 CRC64;
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Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases. The VIRUS TO
-!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO
-!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING
-!- SUBMIT: HOMOTREMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS
-!- SUBMIT: HOMOTREMER. BACH OF THE MONOMERS IS FORMED BY TWO CHAINS
-!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
EMBL; AR270725; AAF82109.1,
-- GO: GO: GO: CIVITAL EMPLOYED: FEA.
                                                                                                                                                       Matrosovich M., Tuzikov A., Bovin N., Gambaryan A., Klimov A., Castrucci M.R., Donatelli I., Kawacka Y., "Early alterations of the receptor-binding properties of H1, H2 and avian influenza virus hemagglutinins after their introduction into
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                                                         Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza A viruses; Influenzavirus A.
NCBI_TaxID=135329;
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Thilluenza A virus (A/Sao Paolo/3/59 (H2N2)).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenza A viruses; Influenzavirus A.
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Last annotation update)
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75.0%; Pred. No. 90;
iive 1; Mismatches 1;
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InterPro; IRR008880; Capsid hemag.
InterPro: PR001364; Hemagglutn.
Pfam; PF00509; Hemagglutinin, 1.
PRINTS; PR00329; HEMAGGLUTNI2.
ProDom; P0000225; Hemagglutn; 1.
Browelope protein; Glycoprotein; Hemagglutinin.
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Hemagglutinin (Fragment).
Influenza A virus (A/RI/5-/57 (H2N2)).
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01-0CT-2000 (TEMBLrel. 15, Last seq
01-0CT-2003 (TEMBLrel. 25, Last ann
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Matches 6; Conserv
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cui-curron: HEMAGGIUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION (BY SIMILARITY).

cui-curron: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (Cui-curron): HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (Cui-curron): HOMOTRIMER BY A DISULFIDE BOND (BY SIMILARITY).

cui-curron: HAZJ0727; AAF8211.1.;

cui-curron: HEMAGGIU-CIVIA HOMOTRIMER IS ARTICALININ FAMILY.

REMBL; ARZ70727; AAF8211.1.;

cui-curron: HEMAGGIU-CIVIA HOMOTRIMER IS ARTICALININ FAMILY.

REMBL; FROOSSOS; HEMAGGIULINI.

REMBL; PROOSSOS; HEMAGGIU
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Matrosovich M., Tuzikov A., Bovin N., Gambaryan A., Klimov A., Castrucci M.R., Donatelli I., Kawaoka Y.;
Mary alterations of the receptor-binding properties of H1, H2 and avian influenza virus hemagglutinins after their introduction into mammals.";
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                                                                                                                                            Length 339;
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Thiluenza A virus (A/Ohio/2/59 (HZNZ)).
Viruses; SSRNA negative-strand viruses; Orthomyxoviridae; Influenza A viruses; Influenzavirus A.
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     339 339 37895 MW; 97D69D60CD5AFD08 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                 Que'ry Match 77.8%; Score 35; DB 12; Best Local Similarity 75.0%; Pred. No. 90; Matches 6; Conservative 1; Mismatches 1
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75.0%; Pred. No. 90;
Live 1; Mismatches
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Best Local Similarity 75.0
Matches 6; Conservative
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